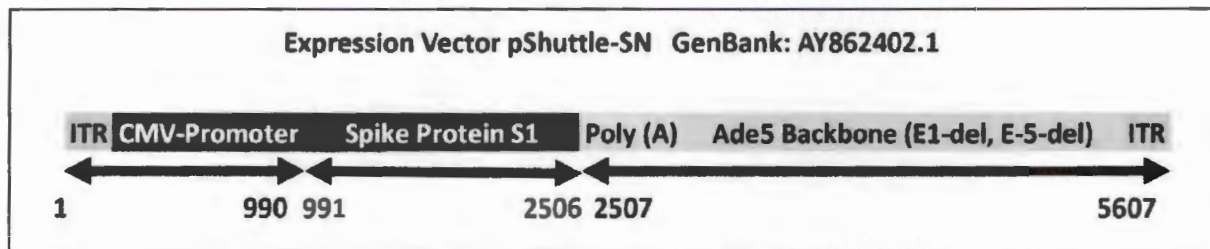


**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

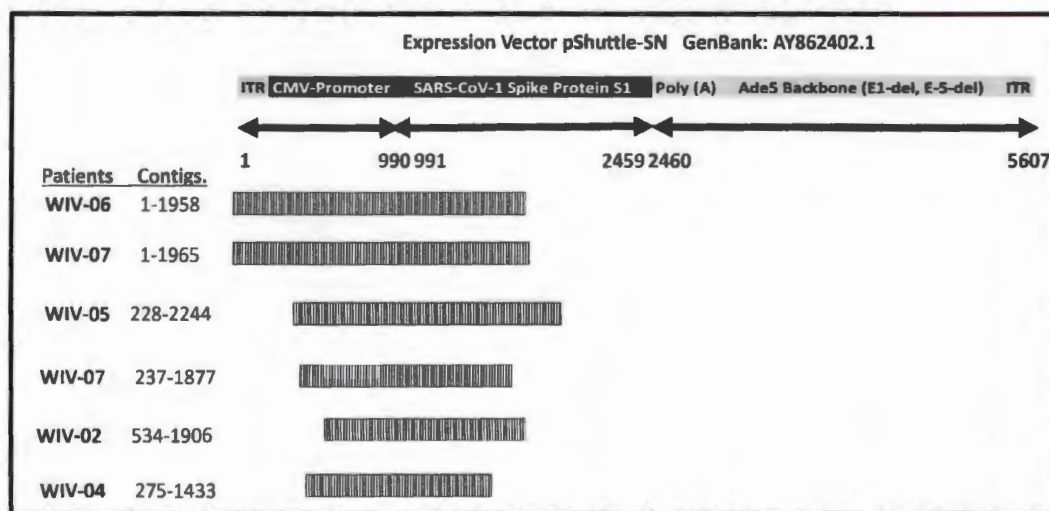
29 January 2021

According to Liu: “Adeno-X™ expression system (Clontech Laboratories, Inc.), comprising adenovirus type 5 genome with a deletion in the E1 and E3 regions ( $\Delta E1$ , 343–3465 bp;  $\Delta E3$ , 28,756–30,561 bp), was utilized to construct a recombinant adenovirus carrying nucleotides –45 to 1469 of Spike gene of SARS-CoV (Ad-SN) by *in vitro* ligation. This provides an immunogen which encoded a truncated S1 subunit of SARS-CoV S protein (490 N-terminal amino-acid residues),” as shown here:



The expected result would be the finding of RNA-Seq sequence raw reads that were homologous to the two Adenovirus regions but only partially homologous (about 80%) to the SARS-CoV-1 regions.

The results are shown below. All five patients have adenovirus sequences that read through the 5' junction with the immunogen but do not read through the entire gene:



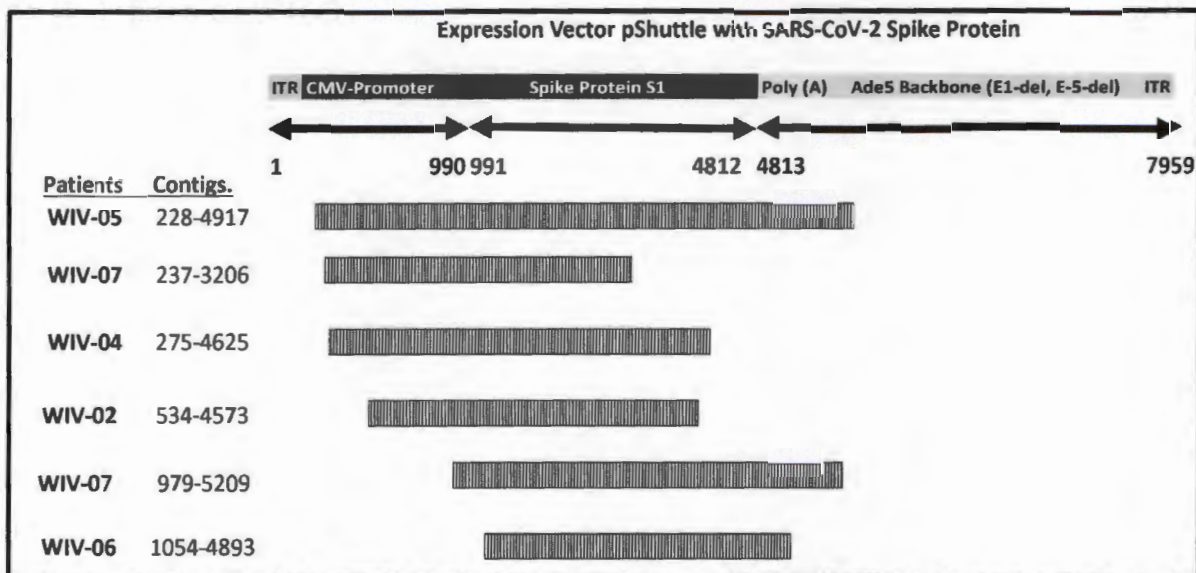
# **Bayesian Analysis of SARS-CoV-2 Origin**

Steven C. Quay, MD, PhD

29 January 2021

As can be seen above, all five patients have significant portions of the CMV-promoter as well as almost one-half of the truncated Spike Protein gene. This is the expected result if in fact the vaccine was not the previously described SARS-CoV-1, as in that case you would expect through reads covering the entire spike protein gene.

Next, an adenovirus vaccine vector sequence was created by substituting the full CoV-2 spike protein gene into the vector cassette. The results for this construct was much greater coverage within the specimens.



For example, the sequence alignment of patient WIV-05 is shown below. The red arrow and green arrow are at the 5' and 3' junctions of the adenovirus vector sequences and the CoV-2 Spike Protein gene sequence, showing cross junction contigs.





**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

29 January 2021

- ☐ **RNA-Seq of Homo sapiens: hCov-19 infected patients Bronchoalveolar lavage uid**  
 1. 1 ILLUMINA (Illumina MiSeq) run: 5.8M spots, 1.7G bases, 634.3Mb downloads  
 Accession: SRX8032203
- ☐ **RNA-Seq of Homo sapiens: hCov-19 infected patients Bronchoalveolar lavage uid**  
 2. 1 ILLUMINA (Illumina MiSeq) run: 5.2M spots, 1.6G bases, 583.4Mb downloads  
 Accession: SRX8032202
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 3. 1 ILLUMINA (Illumina MiSeq) run: 5.2M spots, 1.5G bases, 772.9Mb downloads  
 Accession: SRX7730887
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 4. 1 ILLUMINA (Illumina MiSeq) run: 5.2M spots, 1.5G bases, 768.3Mb downloads  
 Accession: SRX7730886
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 5. 1 ILLUMINA (Illumina MiSeq) run: 8.3M spots, 2.2G bases, 1.2Gb downloads  
 Accession: SRX7730885
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 6. 1 ILLUMINA (Illumina HiSeq 3000) run: 38.5M spots, 11.5G bases, 7.1Gb downloads  
 Accession: SRX7730884
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 7. 1 ILLUMINA (Illumina HiSeq 3000) run: 29.7M spots, 8.9G bases, 5.8Gb downloads  
 Accession: SRX7730883
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 8. 1 ILLUMINA (Illumina HiSeq 3000) run: 34.3M spots, 10.3G bases, 6.4Gb downloads  
 Accession: SRX7730882
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 9. 1 ILLUMINA (Illumina HiSeq 1000) run: 61.3M spots, 18.4G bases, 11.4Gb downloads  
 Accession: SRX7730881
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 10. 1 ILLUMINA (Illumina HiSeq 3000) run: 67.1M spots, 20.1G bases, 12.6Gb downloads  
 Accession: SRX7730880
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
 11. 1 ILLUMINA (Illumina MiSeq) run: 3.6M spots, 1G bases, 548.1Mb downloads  
 Accession: SRX7730879

The WIV entry with the greatest read depth, Number 10 above, is described below:

# Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021

## SRX7730880: RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid

1 ILLUMINA (Illumina HiSeq 3000) run: 67.1M spots, 20.1G bases, 12.6Gb downloads

**Design:** Total RNA was extracted from bronchoalveolar lavage fluid using the QIAamp Viral RNA Mini Kit (50) following the manufacturers instructions. An RNA library was then constructed using the MGIEasy RNA Library Prep Set (96 RXN) (Cat. No.: 1000006384). Paired-end (150 bp sequencing of the RNA library was performed on the MGISEQ-2000RS platform .

**Submitted by:** Wuhan Institute of Virology, Chinese Academy of Sciences

**Study:** Severe acute respiratory syndrome coronavirus 2 Raw sequence reads

[PRJNA605983](#) • [SRP249613](#) • [All experiments](#) • [All runs](#)

[show Abstract](#)

### Sample:

[SAMN14082196](#) • [SRS6151291](#) • [All experiments](#) • [All runs](#)

**Organism:** [Severe acute respiratory syndrome coronavirus 2](#)

### Library:

**Name:** WIV02-2

**Instrument:** Illumina HiSeq 3000

**Strategy:** RNA-Seq

**Source:** METAGENOMIC

**Selection:** RANDOM

**Layout:** PAIRED

**Runs:** 1 run, 67.1M spots, 20.1G bases, 12.6Gb

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR11092063</a>	67,083,195	20.1G	12.6Gb	2020-02-16

Unexpectedly, over 100 sequences producing significant alignment were identified:

BLAST - blastn suite-SRA - results for RID-S76CAHY001R

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How to read this report? BLAST Help Videos Back to Traditional Results Page

Job Title [gb\(A7962402.1\)](#)

RID [S76CAHY001R](#) search expires on 10-11-21 at 11 am Download All

Program BLASTN Citation

Database SRA See details

Query ID [AY862402.1](#)

Description Expression vector pShuttle-SH, complete sequence

Molecule type nucleic acid

Query Length 5607

Other reports Distance tree of results MSA viewer

Descriptions Graphic Summary Alignments

Sequences producing significant alignments Download Manage Columns Show 100

☒ select all 298 sequences selected

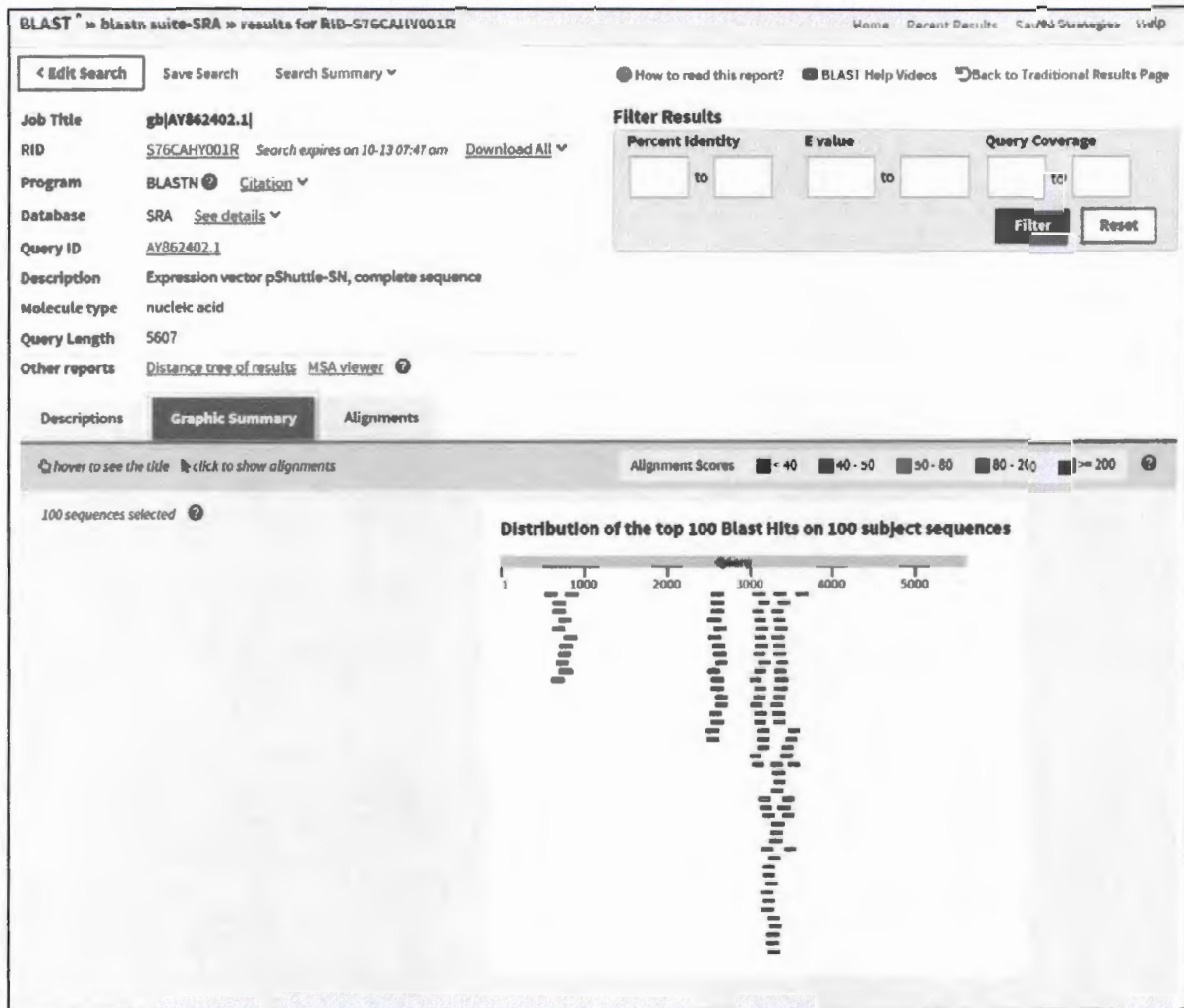
Graphics Distance tree of results

Description	Max Score	Total Score	Query Cover	E value	Pos. Ident	Accession
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<input checked="" type="checkbox"/> <a href="#">SRX7730880</a>	278	278	2%	2e-70	100.00%	<a href="#">SRA-SRR11092063.66604450.95</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730880</a>	278	278	2%	2e-70	100.00%	<a href="#">SRA-SRR11092063.66604</a>

**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

29 January 2021

A graphical display of the alignments shows they are not in the Spike Protein region (961 to 2507) of the adenovirus vector but outside of those regions.



An examination of individual reads show 100% homology over the entire 150 nt segments and outside of the Spike Protein region. The first set of reads are immediately downstream of the Spike Protein segment. The other read is from the region is from the 5' boundary of the Adenovirus vector with the Spike Protein region.





Bayesian Analysis of SARS-CoV-2 Origin  
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29 January 2021

Download

Graphics

SRA

SRX7730880

Sequence ID: SRA:SRR11092063.50609371.2

Length: 150

Number of Matches: 1

Range 1: 1 to 150

Graphics

Next Match

Previous Match

Score	Expect	Identities	Gaps	Strand
278 bits(150)	2e-70	150/150(100%)	0/150(0%)	Plus/Plus
Query 703	CAAGTCTCCACCCATTGACGTCAATGGGAGTTTGT	TTTGGCACCAAAATCAACGGGACT	762	
Sbjct 1	CAAGTCTCCACCCATTGACGTCAATGGGAGTTTGT	TTTGGCACCAAAATCAACGGGACT	60	
Query 763	TTCCAAATGTCGTAACAACCTCCGCCCAT	TGACGCAAATGGGCGGTAGGCGTGTACGGT	822	
Sbjct 61	TTCCAAATGTCGTAACAACCTCCGCCCAT	TGACGCAAATGGGCGGTAGGCGTGTACGGT	120	
Query 823	GGGAGGTCTATATAAGCAGAGCTCTCTGGC	852		
Sbjct 121	GGGAGGTCTATATAAGCAGAGCTCTCTGGC	150		

Download

Graphics

SRA

SRX7730880

Sequence ID: SRA:SRR11092063.50609371.1

Length: 150

Number of Matches: 1

Range 1: 1 to 150

Graphics

Next Match

Previous Match

Score	Expect	Identities	Gaps	Strand
278 bits(150)	2e-70	150/150(100%)	0/150(0%)	Plus/Minus
Query 784	CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAG	843		
Sbjct 150	CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAG	91		
Query 844	CTCTCTGGCTAACTAGAGAACCCTGCTTACTGGCTTATCGAAATTAATACGACTCACT	903		
Sbjct 90	CTCTCTGGCTAACTAGAGAACCCTGCTTACTGGCTTATCGAAATTAATACGACTCACT	31		
Query 904	ATAGGGAGACCCAAGCTGGCTAGCGTTTAA	933		
Sbjct 30	ATAGGGAGACCCAAGCTGGCTAGCGTTTAA	1		

To test if this was the actual SARS-CoV-1 vaccine vector and had been given to the patients as an desperate attempt to create immunity during an infection, the Spike Protein region of the vaccine was blasted against the above sample, looking for a near 100% homology. The only reads were a 38 nt segment of 1482-1518, with one gap, as expected. The absence of long reads for the SARS-CoV-1 Spike Protein suggests that this vaccine was not a CoV-1 vaccine.



Bayesian Analysis of SARS-CoV-2 Origin  
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To test if the homology seen between lavage specimens of patients in Wuhan with the CoV-1 Adenovirus vaccine was due to homology with human sequences the Expression vector was blasted against *Homo sapien* sequences, but no matches were found, as shown below.

**BLAST<sup>®</sup> » blastn suite » results for RID-S793VKCV01R**

[< Edit Search](#)
[Save Search](#)
[Search Summary ▼](#)

**i** Your results are filtered to match records that include: *Homo sapiens* (taxid:9606)

<b>Job Title</b>	<b>AY862402:Expression vector pShuttle-SN, complete...</b>		
<b>RID</b>	<a href="#">S793VKCV01R</a>	Search expires on 10-13 08:34 am	<a href="#">Download All ▼</a>
<b>Program</b>	<a href="#">?</a>	<a href="#">Citation ▼</a>	
<b>Database</b>	nt	<a href="#">See details ▼</a>	
<b>Query ID</b>	<a href="#">AY862402.1</a>		
<b>Description</b>	Expression vector pShuttle-SN, complete sequence		
<b>Molecule type</b>	nucleic acid		
<b>Query Length</b>	5607		
<b>Other reports</b>	<a href="#">?</a>		

**!** No significant similarity found. For reasons why, [click here](#)

**Background.** Live attenuated adenovirus vectors for vaccine or gene therapy have been under development for decades.<sup>139</sup> Adenovirus vaccines against SARS-CoV-1<sup>140</sup> and MERS<sup>141</sup> have shown efficacy in animal models of disease. One of the earliest vaccines for CoV-2 is also an adenovirus vector vaccine, developed in collaboration with the PLA.<sup>142</sup>

<sup>139</sup> <https://www.sciencedirect.com/science/article/pii/S1525001604013425>

<sup>140</sup> <https://www.sciencedirect.com/science/article/pii/S0140673603149628>

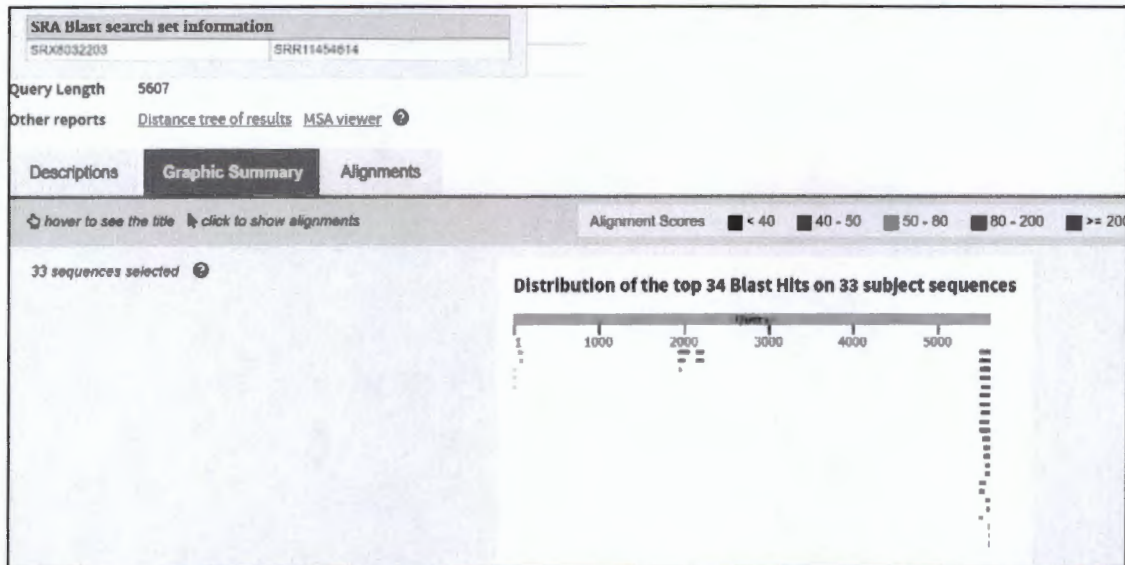
<sup>141</sup> <https://www.nih.gov/news-events/news-releases/investigational-chimp-adenovirus-mers-cov-vaccine-protects-monkeys>

<sup>142</sup> <https://www.nature.com/articles/d41586-020-02523-x> ; <https://www.nature.com/articles/s41467-020-18077-5>

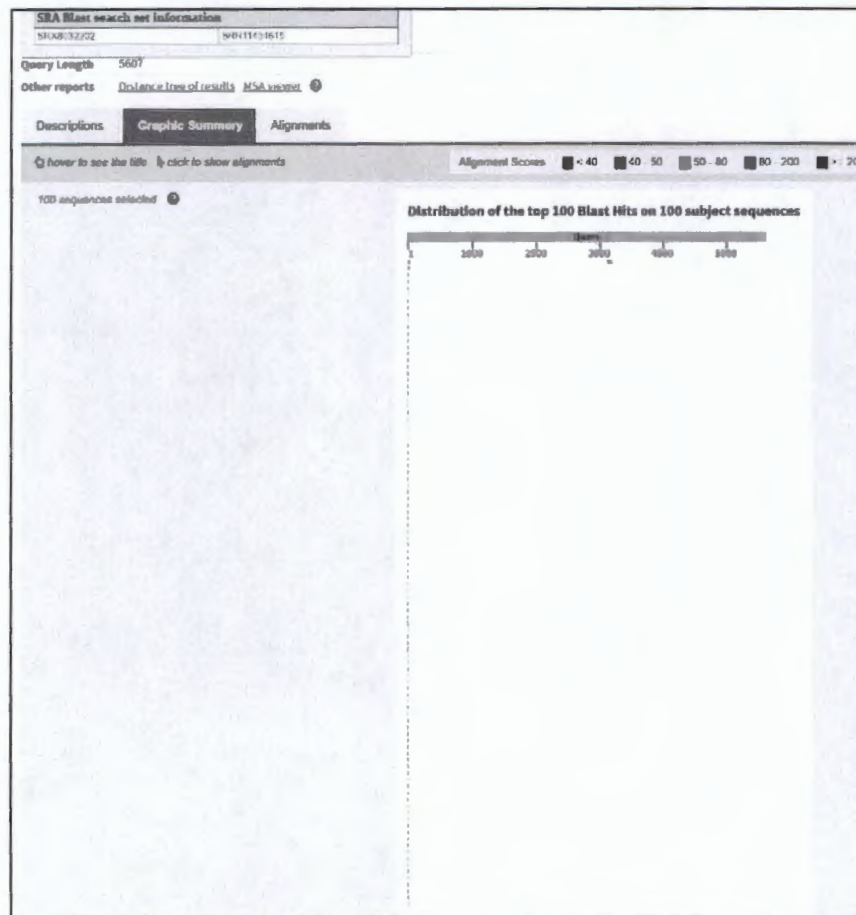
**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

**29 January 2021**

Below is a blast for sequences from the patients in the same hospital who had lavage on the same day but whose specimens went to the Hubei CDC. There are no adenovirus sequences below.



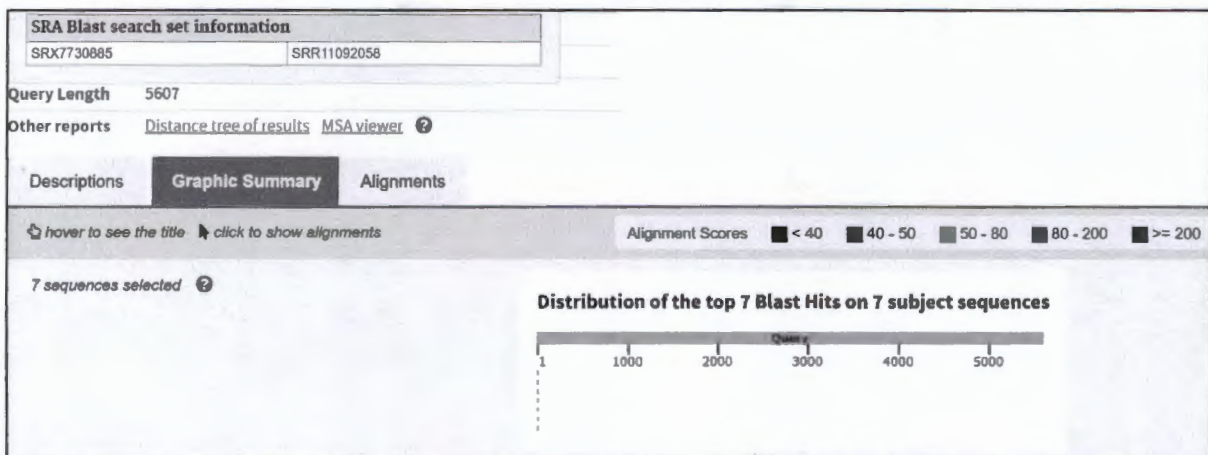
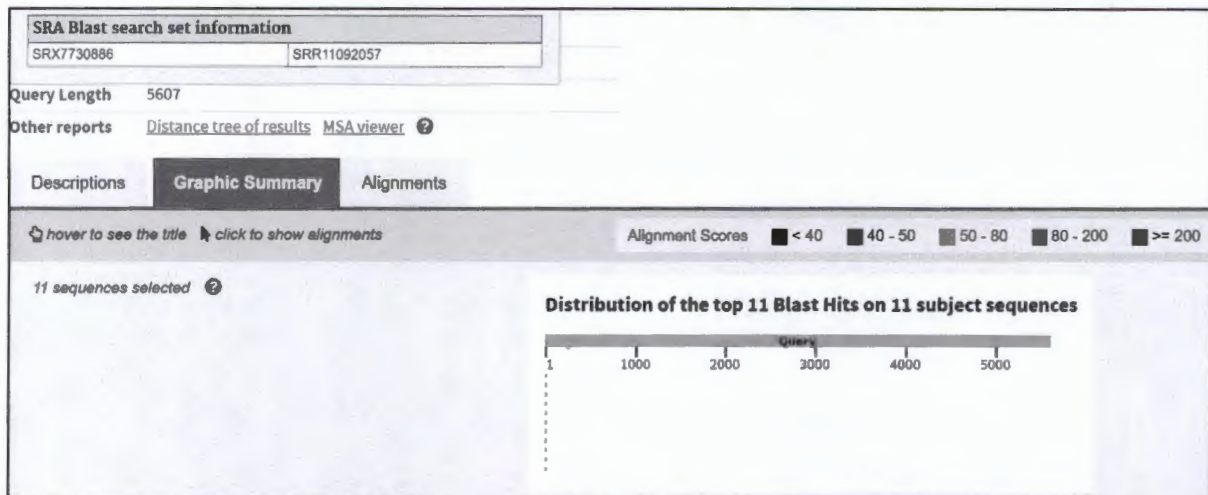
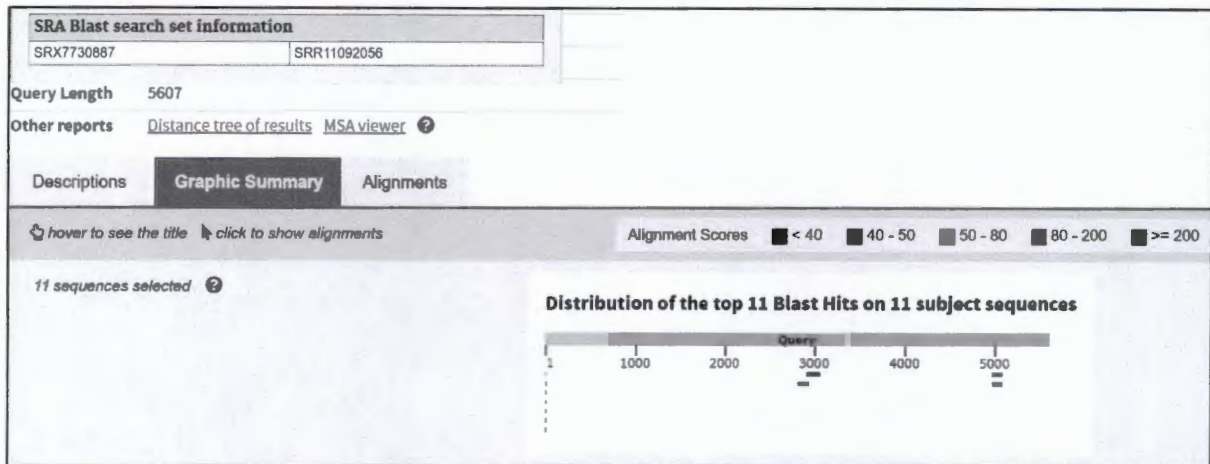
Or in this specimen.



**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

29 January 2021

Or in these specimens.

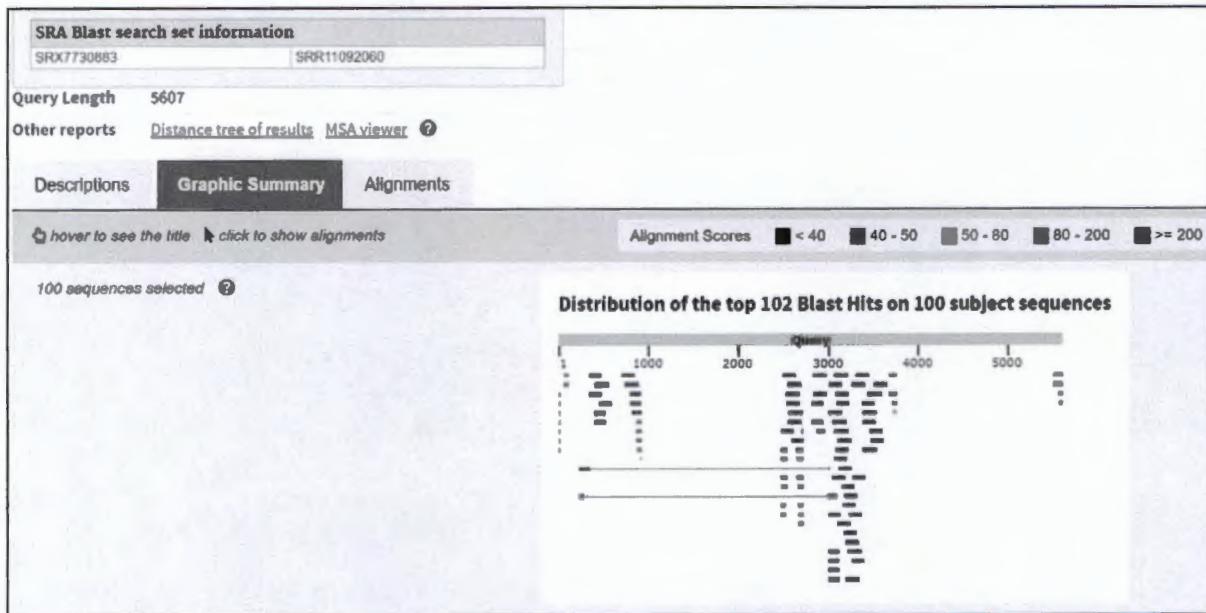
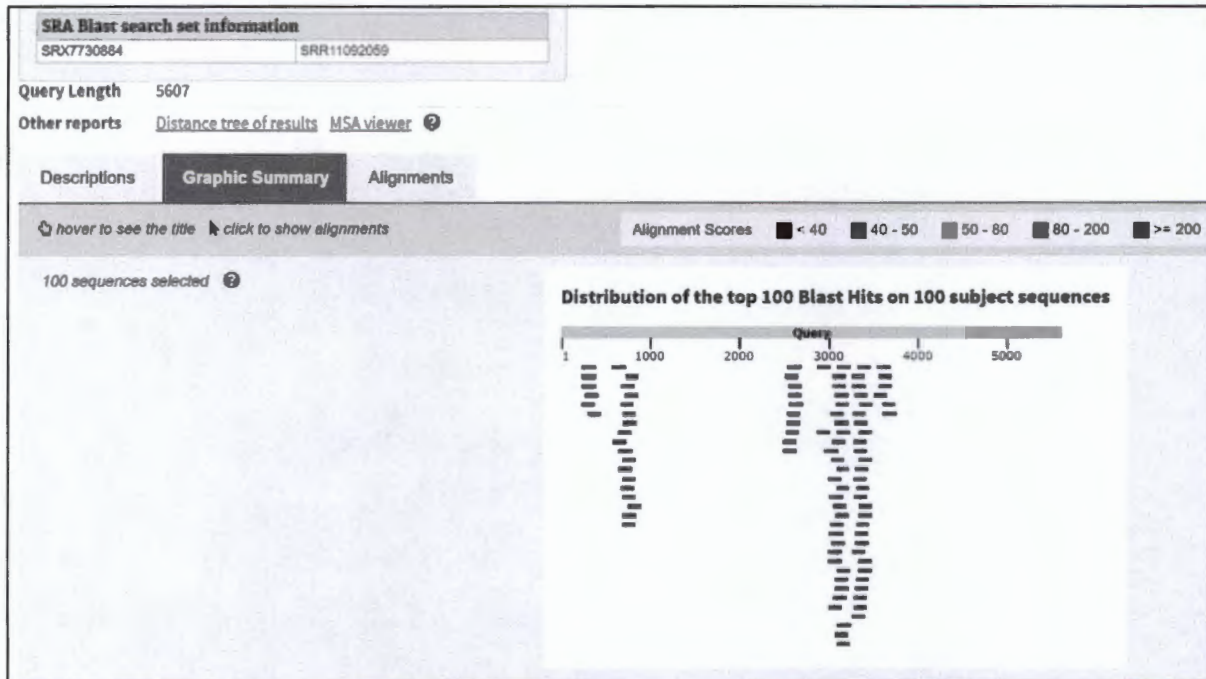




**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

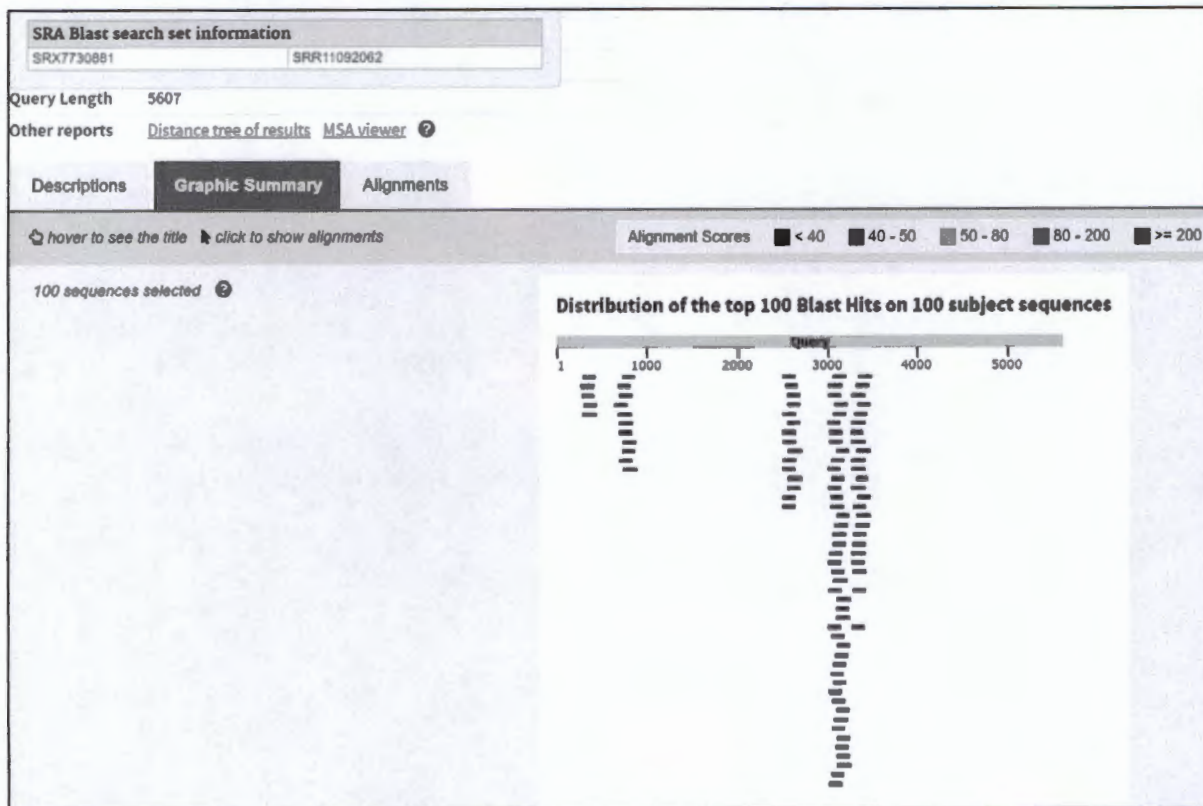
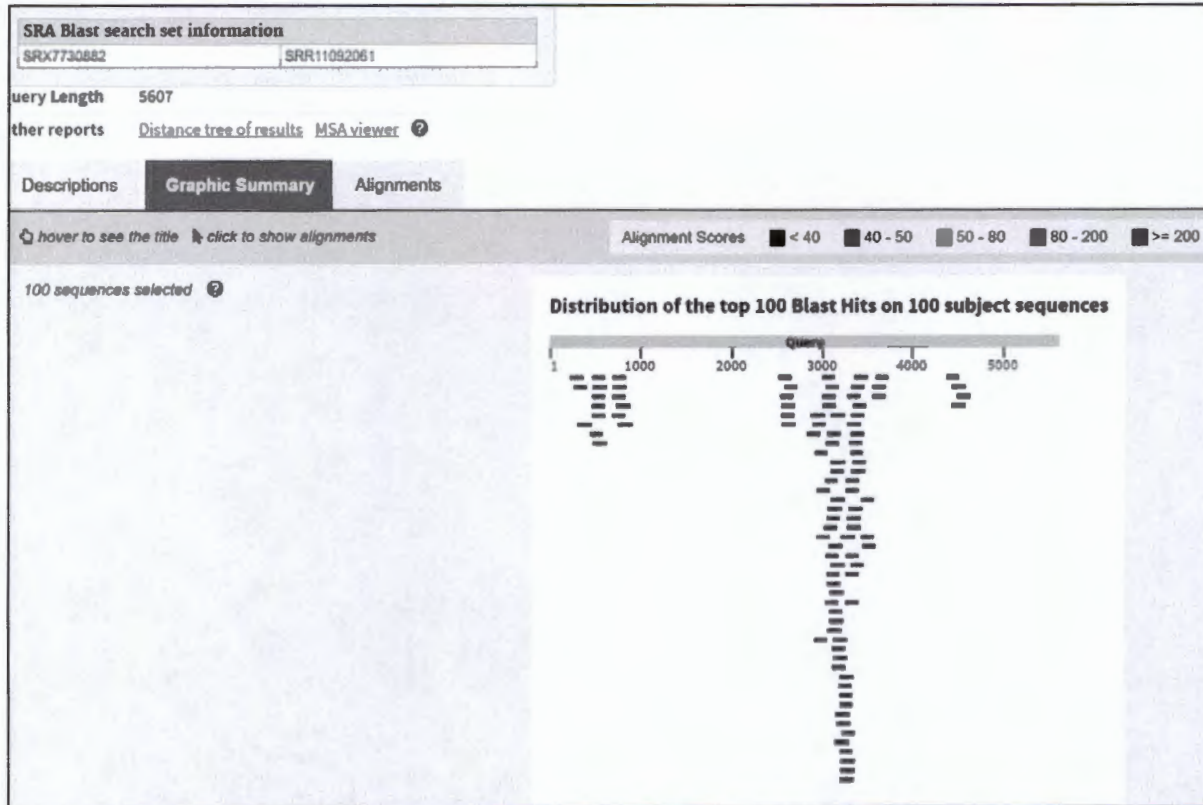
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Below begins the specimens from the WIV.



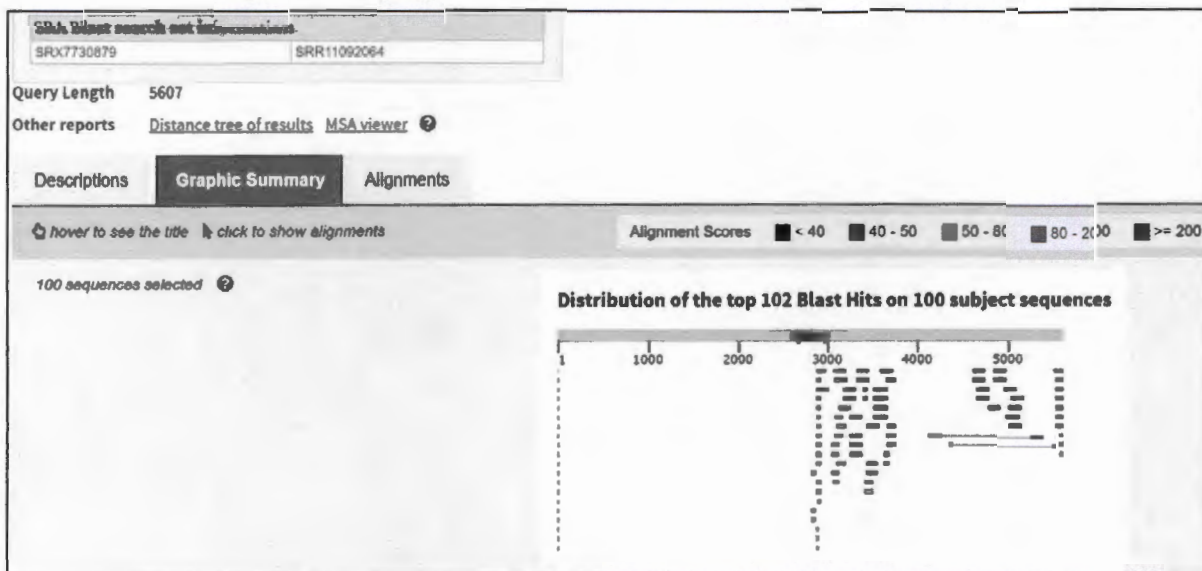
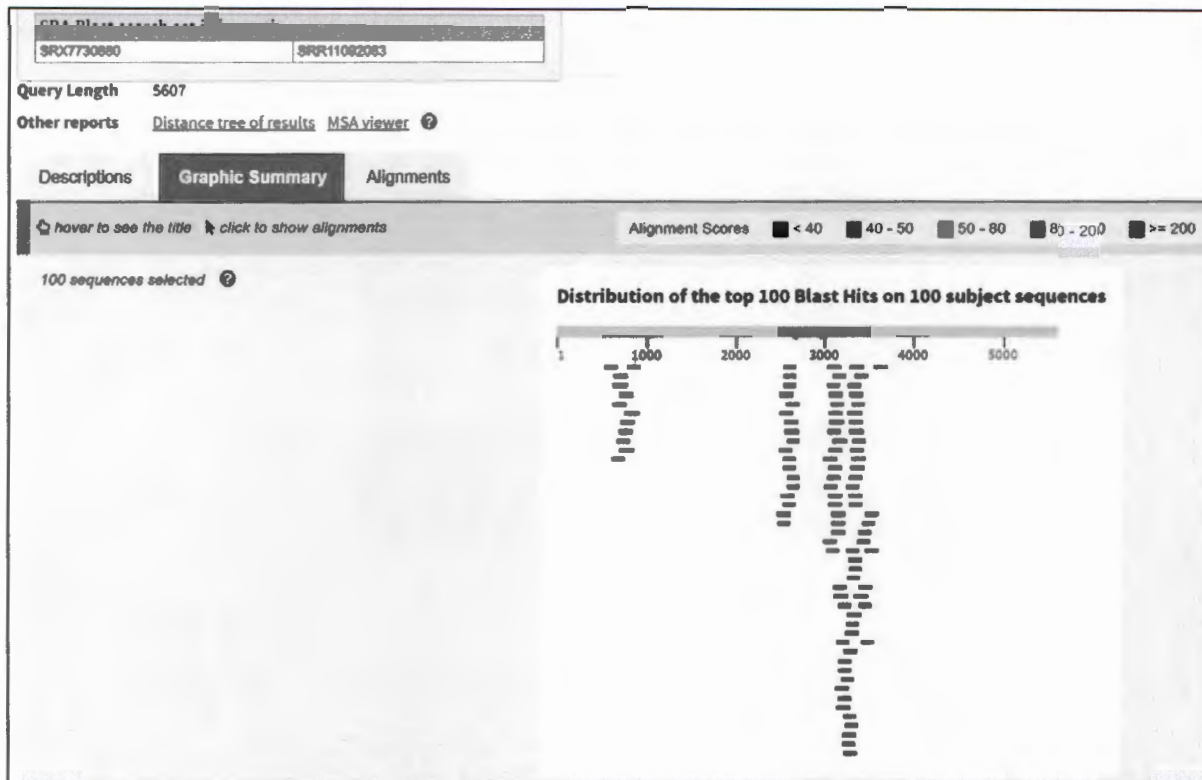
Bayesian Analysis of SARS-CoV-2 Origin  
Steven C. Quay, MD, PhD

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Bayesian Analysis of SARS-CoV-2 Origin  
Steven C. Quay, MD, PhD

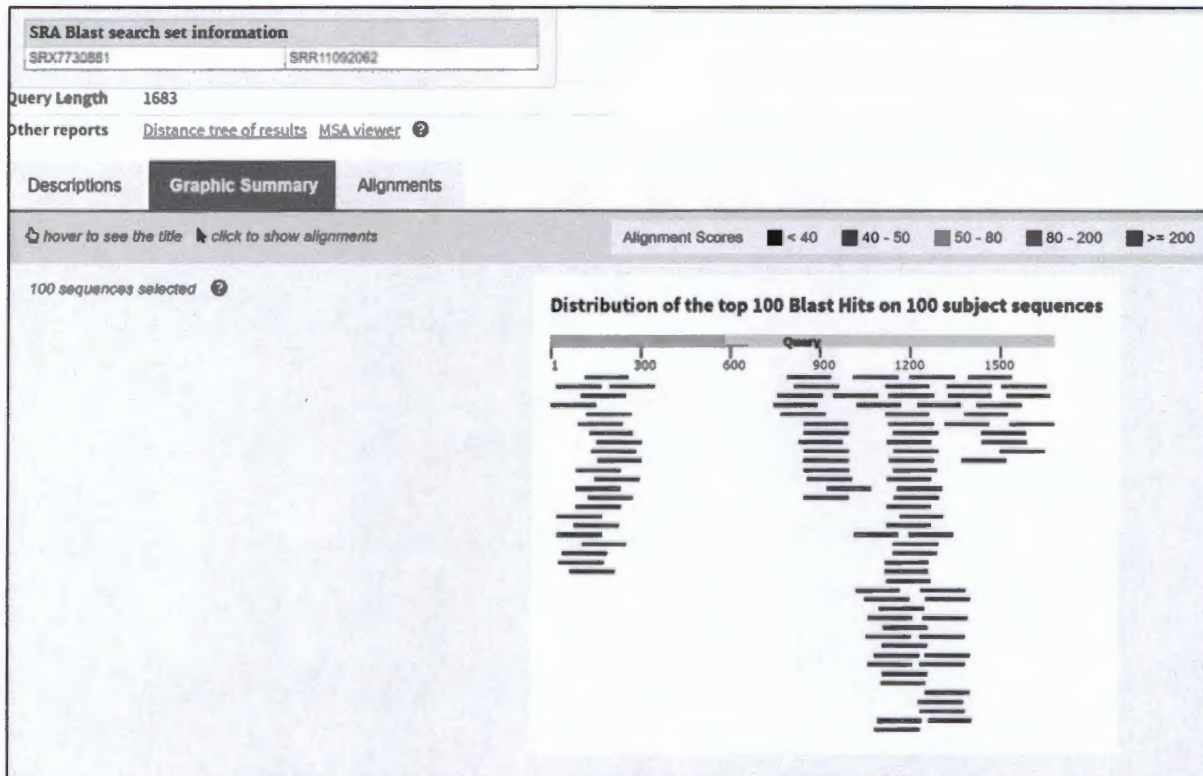
29 January 2021





**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

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Above is a blast of Influenza A virus (A/swine/eastern China/HH24/2017(H7N9)) segment 4 hemagglutinin (HA) gene, complete cds in patient WIV-4-2 specimen

[https://www.ncbi.nlm.nih.gov/nucleotide/MG925503.1?report=genbank&log\\$=nuclalign&blast\\_rank=2&RID=WYG74MH9016](https://www.ncbi.nlm.nih.gov/nucleotide/MG925503.1?report=genbank&log$=nuclalign&blast_rank=2&RID=WYG74MH9016)

<https://www.ncbi.nlm.nih.gov/nuccore/AY862402.1> Expression vector pShuttle-SN, complete sequence

AY862402.1

**Specimen 1**

[https://www.ncbi.nlm.nih.gov/sra/SRX7730879\[accn\]](https://www.ncbi.nlm.nih.gov/sra/SRX7730879[accn])

<https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR11092064>

## Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021

**SRX7730879: RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
1 ILLUMINA (Illumina MiSeq) run: 3.6M spots, 1G bases, 548.1Mb downloads

**Design:** Total RNA was extracted from bronchoalveolar lavage fluid using the QIAamp Viral RNA Mini Kit (50) following the manufacturers instructions. An RNA library was then constructed using the NEBNext Ultra II Directional RNA Kit (NEB, USA). Paired-end (150 bp) sequencing of the RNA library was performed on the MiSeq platform (Illumina).

**Submitted by:** Wuhan Institute of Virology, Chinese Academy of Sciences

**Study:** Severe acute respiratory syndrome coronavirus 2 Raw sequence reads  
[PRJNA605983](#) • [SRP249613](#) • [All experiments](#) • [All runs](#)

[View Abstract](#)  
Discovery and characterization of a novel human coronavirus from five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak .

**Sample:**  
[SAMN14082200](#) • [SRR56151290](#) • [All experiments](#) • [All runs](#)  
Organism: [Severe acute respiratory syndrome coronavirus 2](#)

**Library:**  
Name: WV07  
Instrument: Illumina MiSeq  
Strategy: RNA-Seq  
Source: METAGENOMIC  
Selection: RANDOM  
Layout: PAIRED

**Runs:** 1 run, 3.6M spots, 1G bases, 548.1Mb

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR11092064</a>	3,586,583	1G	548.1Mb	2020-02-15

ID: 10109892

BLAST<sup>®</sup> » blastn suite-SRA » results for RID-5BB5ZMXM01R

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**Job Title** AY862402:Expression vector pShuttle-SN, complete...  
**RID** [5BB5ZMXM01R](#) Search expires on 10-14 21:33 pm [Download All](#) [Filter Results](#)

**Program** BLASTN [Citation](#) [Filter Results](#)

**Database** SRA [See details](#)

**Query ID** [AY862402.1](#)

**Description** Expression vector pShuttle-SN, complete sequence

**Molecule type** nucleic acid

**Query Length** 5607

**Other reports** [Distance tree of results](#) [MSA viewer](#)

**Descriptions** **Graphic Summary** **Alignments**

**Sequences producing significant alignments** [Download](#) [Manage Columns](#) [Show 100](#)

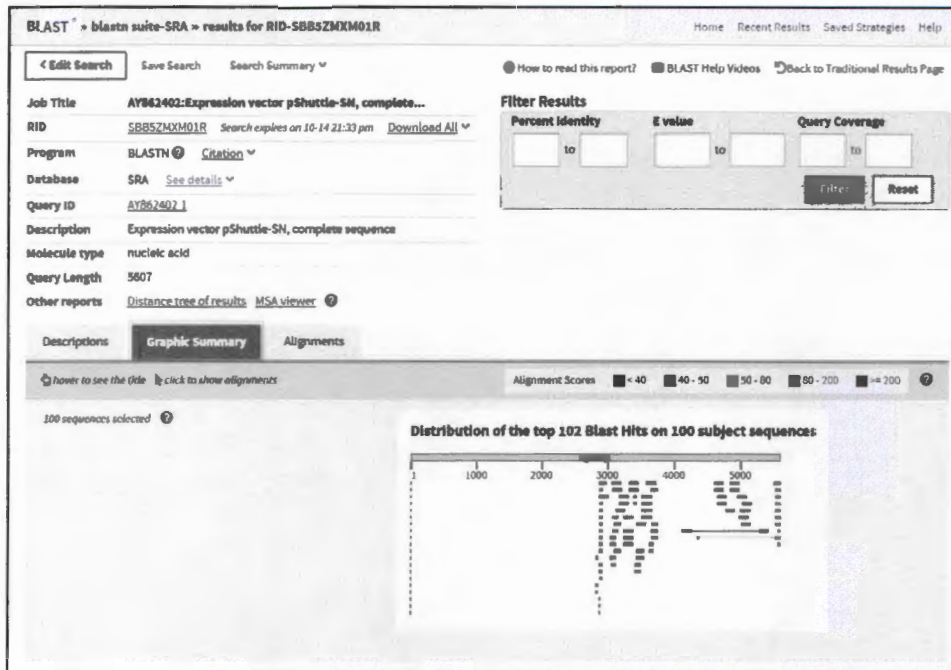
☒ select all 100 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.3312575.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.2817503.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.2878881.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.2878881.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.2855759.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.2415875.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.1594732.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	2e-72	100.00%	<a href="#">SRA:SRX11092064.1313017.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	279	279	2%	9e-72	100.00%	<a href="#">SRA:SRX11092064.3612575.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	278	278	2%	9e-72	100.00%	<a href="#">SRA:SRX11092064.2415875.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	278	278	2%	9e-72	100.00%	<a href="#">SRA:SRX11092064.1313017.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	276	276	2%	9e-71	100.00%	<a href="#">SRA:SRX11092064.2868099.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	274	274	2%	1e-70	99.34%	<a href="#">SRA:SRX11092064.1428185.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	274	274	2%	1e-70	99.34%	<a href="#">SRA:SRX11092064.1428185.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	274	274	2%	1e-70	99.34%	<a href="#">SRA:SRX11092064.734472.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	274	274	2%	1e-70	99.34%	<a href="#">SRA:SRX11092064.734472.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	274	274	2%	1e-70	99.34%	<a href="#">SRA:SRX11092064.674542.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	274	274	2%	1e-70	99.34%	<a href="#">SRA:SRX11092064.612814.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	272	272	2%	4e-70	99.33%	<a href="#">SRA:SRX11092064.674542.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	268	268	2%	5e-69	98.66%	<a href="#">SRA:SRX11092064.2817500.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	268	268	2%	6e-69	98.66%	<a href="#">SRA:SRX11092064.2855759.1</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	267	267	2%	2e-68	98.67%	<a href="#">SRA:SRX11092064.612514.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	266	266	2%	3e-68	99.30%	<a href="#">SRA:SRX11092064.5189732.2</a>
<input checked="" type="checkbox"/> <a href="#">SRX7730879</a>	266	266	2%	3e-68	99.30%	<a href="#">SRA:SRX11092064.5189732.1</a>

## Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021





## Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021

## SRX7730879

Sequence ID: [SRA:SRR11092064.3512575.2](#) Length: 151 Number of Matches: 1Range 1: 1 to 151 [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
279 bits(151)	2e-72	151/151(100%)	0/151(0%)	Plus/Minus
Query 4830	ACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTA	4889		
Sbjct 151	ACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTA	92		
Query 4890	CGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATCCGTCAGCCAGTTTAGTCTGACC	4949		
Sbjct 91	CGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATCCGTCAGCCAGTTTAGTCTGACC	32		
Query 4950	ATCTCATCTGTAACATCATTGGCAACGCTAC	4980		
Sbjct 31	ATCTCATCTGTAACATCATTGGCAACGCTAC	1		

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## SRX7730879

Sequence ID: [SRA:SRR11092064.2917500.1](#) Length: 151 Number of Matches: 1Range 1: 1 to 151 [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
279 bits(151)	2e-72	151/151(100%)	0/151(0%)	Plus/Minus
Query 3319	CCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAACCCGGT	3378		
Sbjct 151	CCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAACCCGGT	92		
Query 3379	AAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA	3438		
Sbjct 91	AAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA	32		
Query 3439	TGTAGGCGGTGCTACAGAGTTCTTGAAGTGG	3469		
Sbjct 31	TGTAGGCGGTGCTACAGAGTTCTTGAAGTGG	1		

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## SRX7730879

Sequence ID: [SRA:SRR11092064.2878891.2](#) Length: 151 Number of Matches: 1Range 1: 1 to 151 [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
279 bits(151)	2e-72	151/151(100%)	0/151(0%)	Plus/Plus
Query 3059	CATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA	3118		
Sbjct 1	CATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA	60		
Query 3119	AACCCGACAGGACTATAAAGATACGAGGCTTTCCCCCTGGAAGCTCCCTCGTGCCTCT	3178		
Sbjct 61	AACCCGACAGGACTATAAAGATACGAGGCTTTCCCCCTGGAAGCTCCCTCGTGCCTCT	120		
Query 3179	CCTGTTCCGACCCTGCCGCTTACCGGATACC	3209		
Sbjct 121	CCTGTTCCGACCCTGCCGCTTACCGGATACC	151		

## Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021

### Specimen 2

[https://www.ncbi.nlm.nih.gov/sra/SRX7730880\[accn\]](https://www.ncbi.nlm.nih.gov/sra/SRX7730880[accn])

**SRX7730880: RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
1 ILLUMINA (illumina HiSeq 3000) run: 67.1M spots, 20.1G bases, 12.6Gb downloads

**Design:** Total RNA was extracted from bronchoalveolar lavage fluid using the QIAamp Viral RNA Mini Kit (50) following the manufacturers instructions. An RNA library was then constructed using the MGIEasy RNA Library Prep Set (96 RXN) (Cat. No.: 1000006384). Paired-end (150 bp) sequencing of the RNA library was performed on the MGISEQ-2000RS platform .

**Submitted by:** Wuhan Institute of Virology, Chinese Academy of Sciences

**Study:** Severe acute respiratory syndrome coronavirus 2 Raw sequence reads  
[PRJNA605983](#) • [SRP249613](#) • [All experiments](#) • [All runs](#)  
[hide Abstract](#)

Discovery and characterization of a novel human coronavirus from five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak .

**Sample:**  
[SAMN14082196](#) • [SRS6151291](#) • [All experiments](#) • [All runs](#)  
**Organism:** [Severe acute respiratory syndrome coronavirus 2](#)

**Library:**  
**Name:** WIV02-2  
**Instrument:** illumina HiSeq 3000  
**Strategy:** RNA-Seq  
**Source:** METAGENOMIC  
**Selection:** RANDOM  
**Layout:** PAIRED

**Runs:** 1 run, 67.1M spots, 20.1G bases, 12.6Gb

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR11092063</a>	67,083,195	20.1G	12.6Gb	2020-02-16

ID: 10106683

**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

29 January 2021

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**Job Title** gb|AY862402.1|

**RID** SBCKMVDN01R [Search expires on 10-14 21:58 pm](#) [Download All](#)

**Program** BLASTN [Citation](#)

**Database** SRA [See details](#)

**Query ID** AY862402.1

**Description** Expression vector pShuttle-SN, complete sequence

**Molecule type** nucleic acid

**Query Length** 5607

**Other reports** [Distance tree of results](#) [MSA viewer](#)

**Filter Results**

**Percent Identity**  to  **E value**  to  **Query Coverage**  to

[Filter](#) [Reset](#)

**Descriptions** [Graphic Summary](#) [Alignments](#)

**Sequences producing significant alignments** [Download](#) [Manage Columns](#) [Show](#) 100 [Graphics](#) [Distance tree of results](#)

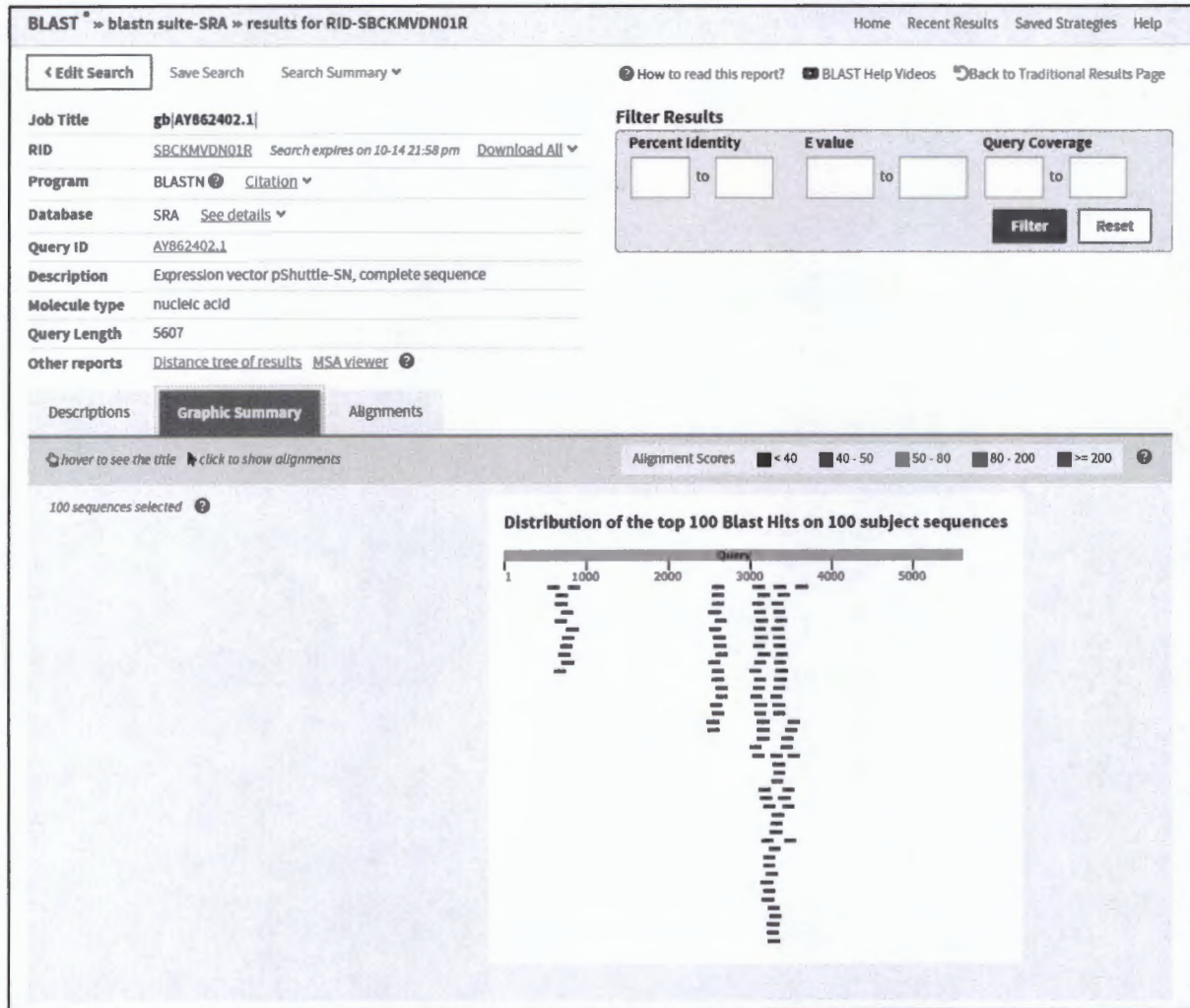
☒ select all 100 sequences selected

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.66604450.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.66455076.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.63120099.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.63120099.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.62730385.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.61105639.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.60748776.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.60011402.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.59155252.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.59155252.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.58125883.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.57571550.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.57484454.2
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<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.55663455.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.55111993.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.53777284.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.53579813.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.52965281.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.5141706.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.51016881.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.50609371.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.50609371.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.49509270.1
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<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.45883858.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.45044544.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.42931446.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.42931446.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.41645159.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.38667194.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.38582435.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.36234753.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.34989436.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.34431070.1
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<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.32257474.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.31163438.2
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.30919310.1
<input checked="" type="checkbox"/>	SRX7730880	278	278	2%	2e-70	100.00%	SRA-SRR11092063.29731694.1



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The above distribution of hits appears to ‘invade’ the antigenic, Spike Protein region of the vaccine, residues 961 to 2507. To determine if this was the case, the hit that contained part of the antigen section was displayed (below).

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<b>SRX7730880</b>					
Sequence ID: <a href="#">SRA:SRR11092063.55111993.2</a> Length: 150 Number of Matches: 1					
Range 1: 1 to 150 <a href="#">Graphics</a> <a href="#">Next Match</a>					
Score	Expect	Identities	Gaps	Strand	
270 bits(146)	3e-68	149/150(99%)	1/150(0%)	Plus/Plus	
Query 2471	GTTTAAA-CCGCTGATCAGCCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTGTTGC				2529
Sbjct 1	GTTTAAACCCGCTGATCAGCCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTGTTGC				60
Query 2530	CCCTCCCCCGTGCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCTTCTTAATAA				2589
Sbjct 61	CCCTCCCCCGTGCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCTTCTTAATAA				120
Query 2590	AATGAGGAAATTGCATCGCATTGTCTGAGT		2619		
Sbjct 121	AATGAGGAAATTGCATCGCATTGTCTGAGT		150		
<a href="#">Download</a> <a href="#">Graphics</a> <a href="#">SRA</a>					
<b>SRX7730880</b>					
Sequence ID: <a href="#">SRA:SRR11092063.54767346.1</a> Length: 150 Number of Matches: 1					
Range 1: 2 to 150 <a href="#">Graphics</a> <a href="#">Next Match</a>					
Score	Expect	Identities	Gaps	Strand	
270 bits(146)	3e-68	148/149(99%)	0/149(0%)	Plus/Plus	
Query 2478	CCGCTGATCAGCCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTGTTGCCCTCCCC				2537
Sbjct 2	CCGCTGATCAGCCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTGTTGCCCTCCCC				61
Query 2538	CGTGCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCTTCTTAATAAAATGAGGA				2597
Sbjct 62	CGTGCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCTTCTTAATAAAATGAGGA				121
Query 2598	AATTGCATCGCATTGTCTGAGTAGGTGTC		2626		
Sbjct 122	AATTGCATCGCATTGTCTGAGTAGGTGTC		150		

As you can see, this 150 nt sequence starts at 2471 and within the antigen segment. However, there is no homology identified when this is blasted against the Reference Sequence of SARS-CoV-2.

### Sample 3

<b>SRX7730881: RNA-Seq of human septans: bronchioloalveolar lavage fluid</b>					
1 ILLUMINA (Illumina HiSeq 1000) run: 61.3M spots, 18.4G bases, 11.4Gb downloads					
Design: Total RNA was extracted from bronchoalveolar lavage fluid using the QiAamp Viral RNA Mini Kit (50) following the manufacturer's instructions. An RNA library was then constructed using the MGIEasy RNA Library Prep Set (96 RDN) (Cat. No.: 1000008384). Paired-end (150 bp) sequencing of the RNA library was performed on the MGISEQ-2000RS platform.					
Submitted by: Wuhan Institute of Virology, Chinese Academy of Sciences					
Study: Severe acute respiratory syndrome coronavirus 2 Raw sequence reads					
<a href="#">PRJNA605963</a> • <a href="#">SRP248613</a> • <a href="#">All experiments</a> • <a href="#">All runs</a>					
Discovery and characterization of a novel human coronavirus from five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak.					
Sample:					
<a href="#">SAMN14082197</a> • <a href="#">SRP6151292</a> • <a href="#">All experiments</a> • <a href="#">All runs</a>					
Organism: <a href="#">Severe acute respiratory syndrome coronavirus 2</a>					
Library:					
Name: WV04-2					
Instrument: Illumina HiSeq 1000					
Strategy: RNA-Seq					
Source: METAGENOMIC					
Selection: RANDOM					
Layout: PAIRED					
Runs: 1 run, 61.3M spots, 18.4G bases, 11.4Gb					
Run	# of Spots	# of Bases	Size	Published	
<a href="#">SRR11092062</a>	61,304,030	18.4G	11.4Gb	2020-02-16	
ID: 10106894					

### Sample 4

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### **SRX7730882: RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**

1 ILLUMINA (Illumina HiSeq 3000) run: 34.3M spots, 10.3G bases, 6.4Gb downloads

**Design:** Total RNA was extracted from bronchoalveolar lavage fluid using the QIAamp Viral RNA Mini Kit (50) following the manufacturers instructions. An RNA library was then constructed using the MGIEasy RNA Library Prep Set (96 RXN) (Cat. No.: 1000006384). Paired-end (150 bp) sequencing of the RNA library was performed on the MGISEQ-2000RS platform .

**Submitted by:** Wuhan Institute of Virology, Chinese Academy of Sciences

**Study:** Severe acute respiratory syndrome coronavirus 2 Raw sequence reads

[PRJNA605983](#) • [SRP249613](#) • [All experiments](#) • [All runs](#)

Discovery and characterization of a novel human coronavirus from five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak .

#### **Sample:**

[SAMN14082198](#) • [SRS6151293](#) • [All experiments](#) • [All runs](#)

**Organism:** [Severe acute respiratory syndrome coronavirus 2](#)

#### **Library:**

**Name:** WIV05

**Instrument:** Illumina HiSeq 3000

**Strategy:** RNA-Seq

**Source:** METAGENOMIC

**Selection:** RANDOM

**Layout:** PAIRED

**Runs:** 1 run, 34.3M spots, 10.3G bases, [6.4Gb](#)

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR11092061</a>	34,255,843	10.3G	6.4Gb	2020-02-16

ID: 10108895

[https://www.ncbi.nlm.nih.gov/sra/SRX2913157\[accn\]](https://www.ncbi.nlm.nih.gov/sra/SRX2913157[accn])

Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College

above has a few 125 nt hits between about 1950 to 3500 in adenovirus



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## Sequences used for the blast analyses

### Adenovirus vaccine with CoV-1 Spike Protein

```
1 taactataac ggtcctaagg tagcgaaage tcagatctgg atctcccgat cccctatggt
61 cgactctcag tacaatctgc tctgatgccg catagttaag ccagtatctg ctccctgctt
121 gtgtgttga ggtcgtcag tagtgcgca gcaaattta agctacaaca aggcaaggct
181 tgaccgacaa ttgatgaag aatctgctta gggtaggcg tttgctgctg ctgcgcatg
241 tacggggccag atatacgcgt tgacattgat tattgactag ttattaatag taatcaatta
301 cgggggtcatt agttcatagc ccatatatgg agttccgcgt tacataactt acggtaaatg
361 gcccgcctgg ctgaccgccc aacgaccccc gccattgac gtcaataatg acgtatgttc
421 ccatagtaac gccaataggg actttccatt gacgtcaatg ggtggactat ttacggtaaa
481 ctgcccactt ggcagtacat caagtgtatc atatgccaag tacgccccct attgacgtca
541 atgacggtaa atggcccgcc tggcattatg ccagttacat gaccttatgg gactttccta
601 cttggcagta catctacgta ttatcatcgt ctattacat ggtgatgcgg ttttggcagt
661 acatcaatgg gcgtggatag cgttttgact cacggggatt tccaagtctc caccctattg
721 acgtcaatgg gagtttgtt tggcaccaaa atcaacggga ctttccaaaa tgtcgttaaca
781 actccgcccc attgacgcaa atggcgcgta ggcgtgtacg gtgggaggtc tatataagca
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901 actataggga gacccaagct ggctagcgtt taaacggggc ctctagagtt gtggtttcaa
961 gtgatattct tgtaataac taaacgaaca tgtttattt ctattattt ctactctca
1021 ctagtggtag tgacctgac cgggtgacca ctttgatga tttcaagct cctaattaca
1081 ctaacatac ttactatag agggggggtt actactctga tgaaatttt agatcagaca
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1201 ctattaatca tacgtttgac aacctgtca taccittaa ggalggatt tattttgctg
1261 ccacagagaa atcaaatgtt gtccgtggtt ggggttttgg ttctaccatg aacaacaagt
1321 cacagtcggt gattattatt aacaattcta ctaatgtgt talacgagca tgaactttg
1381 aattgttga caaccttct tttgctgtt ctaaacccat ggttacacag acacatacta
1441 tgatattega taatgcattt aattgcactt tcagttacat atctgatgcc ttttcgctg
1501 atgtttcaga aaagtcagggt aattttaaac acttacgaga gtttgtgtt aaaaataaag
1561 atgggtttct ctatgtttat aagggtctat aacctataga ttagttcgt gatctacctt
1621 ctggttttaa cactttgaaa cctatttita agttgcctct tggtaatac attacaaatt
1681 tttagagccat tttacagcc ttttacctg cgcaagacac ttggggcacg tcagctgcag
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2161 gagatgatgt aagacaaata gcccaggac aaactggtgt tattgtgat tataattata
2221 aattgccaga tgatttcag gttgtgtgtec ttgcttgaa tactaggaac attgatgcta
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2341 ttgagagaga catatctaata gtgcctttct ccctgatgg caaaccttgc accccacctg
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2461 ccaagcttaa gtttaaacg ctgacagcc tcgactgtgc cttctagttg ccagccatct
```

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2521 gttgtttgcc cctccccctg gccttccttg accctggaag gtgccactcc cactgtcctt  
2581 tcttaataaa atgaggaaat tgcategcat tgtctgagta ggtgtcattc tattctgggg  
2641 ggtgggggtgg ggcaggacag caaggggggag gattgggaag acaatagcag gcatgtctggg  
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3121 cccgacagga ctataaagat accaggcgtt tccccctgga agtccctcg tgcgtctcc  
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3241 gcttttcaa tgctacgct gtaggtatct cagttcgggtg taggtcttc gctcaagct  
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3541 aaaaagagtt ggtagctctt gatccggcaa acaaacacc gctggtagcg gtgtttttt  
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3841 aataaacga accgtacac cctgagcatc aaactcttt atcagttgga tcatgtcggc  
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3961 cactctcagc aaatccagcc ctcccgatc tgttgaactg ccggatgcct tgcggtaaa  
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4981 ctttgccatg tticagaac aactctggcg catcgggctt cccatacaat cgatagattg  
5041 tcgcacctga ttgcccgaca ttatcgagag cccatttata cccatataaa tcagcatcca  
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5161 ccttgtatt actgttatg taagcagaca gttttattgt tcatgatgat atattttat  
5221 cttgtgcaat gtaacatcag agattttgag acacaacgtg gctttgtga ataaatcgaa

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5281 cttttgctga gttgaaggat cagatcacgc atcttcccga caacgcagac cgttccgtgg  
5341 caaagcaaaa gttcaaaatc accaactggt ccacctacaa caaagctctc atcaaccgtg  
5401 gctccctcac ttctggctg gatgatgggg cgattcaggc ctggtatgag tcagcaacac  
5461 cttcttcacg aggcagacct cagcgtaga ttattgaagc atttatcagg gttattgtct  
5521 catgagcggg tacatatttg aatgtattta gaaaaataaa caaatagggg ttccgcgcac  
5581 atttcccga aaagtccac ctgacgt

**SARS-CoV-2 Spike Protein gene**

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21601 tcaagtgtgt aatcttaca ccagaactca attaceccct gcatacacta attcttca  
21661 acgtgggtgt tattacctg acaaagttt cagatctca gttttacatt caactcagga  
21721 cttgttctta cttttcttt ccaatgttac ttggttccat gctatacatg tctctgggac  
21781 caatggtaact aagagggttg ataaccctgt cctaccattt aatgatggtg ttattttgc  
21841 ttccactgag aagtctaaca taataagagg ctggattttt ggtactactt tagattcgaa  
21901 gaccagtcct ctactattg ttaataacgc tactaatgtt gttattaaag tctgtgaatt  
21961 tcaattttgt aatgatecat tttgggtgt ttattaccac aaaaacaaca aaagtggat  
22021 ggaaagtgag ttcagagttt attctagtgc gaataattgc acttttgaat atgtctctca  
22081 gccctttctt atggaccttg aaggaaaaca gggtaatttc aaaaactta gggaattgt  
22141 gtttaagaat atgatgggt atttataaat atattctaag cacacgcta ttaatttagt  
22201 gcgtgatctc cctcagggtt ttccggcttt agaaccattg gtagatttgc caataggtat  
22261 taacatcact aggtttcaaa ctttacttgc ttacataga agttatttga ctctgggtga  
22321 ttcttctca ggttggacag ctggttctgc agcttattat gtgggttctc tcaacctag  
22381 gacttttcta ttaaaatata atgaaaatgg aaccattaca gatgctgtag actgtgcaat  
22441 tgacctctc tcagaaacaa agtgtacgtt gaaatcctc actgtagaaa aaggaatcta  
22501 tcaaacttet aactttagag tcaaaccaac agaactattt gttagatttc ctaattattc  
22561 aaacttgtgc ctttttggg aagtttttaa cgcaccaga ttgcacttg ttatgcttg  
22621 gaacaggaag agaatcagca actgtgttgc tgattattct gtctatata attccgcatc  
22681 attttccact ttaagtgtt atggagtgc tctactaaa ttaaatgate tctgctttac  
22741 taatgtctat gcagattcat ttgtaattag aggtgatgaa gtcagacaaa tctctccagg  
22801 gcaaactgga aagattgtc attataatta taaattacca gatgatttca caggctgcgt  
22861 tatagcttgg aattctaaca atcttgatc taaggtttgt ggtaattata attacctgta  
22921 tagattgttt aggaagtcta atctcaaac tttgagaga gatatttcaa ctgaaatcta  
22981 tcaggccggt agcacacctt gtaatgggtt tgaaggtttt aattgttact ttctttaca  
23041 atcatatggt ttcaacca ctaatgggtt tggttacca ccatcacagag tagtagtact  
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23221 tgagtctaac aaaaagttc tgctttcca acaatttggc agagacattg ctgacactac  
23281 tgatgtctgc cgtgatccac agacacttga gattcttgac attacacat gttcttttgg  
23341 tgggtgtaag gttataacac caggaacaaa tacttctaac cagggttctg ttctttatca  
23401 ggatgttaac tgcacagaag tccctgttgc tattcatgca gatcaactta ctctacttgc  
23461 gcgtgtttat tctacaggtt ctaatgttt tcaaacacgt gcaggctgtt taataggggc  
23521 tgaacatgac acaactcat atgagtgtga cataccattt ggtgcaggta tatgcgctag  
23581 ttatcagact cagactaatt ctctcggcgg ggcacgtagt gtagctagtc aatccatcat  
23641 tgcctacact atgtcacttg gtgcagaaaa ttcaattgtc tactctaata actctattgc  
23701 cataccaca aattttacta ttagtgttac cacagaaatt ctaccagtgt ctatgacca



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23761 gacatcagta gattgtacaa tglacatttg tgggtattca actgaatgca gcaatctttt  
23821 gttgcaatat ggcagttttt glacacaatt aaaccgtget ttaactggaa tagctgttga  
23881 acaagacaaa aacacceaaag aagtttttgc acaagtcaaa caaatftaca aaacaccacc  
23941 aattaaagat ttgggtggtt ttaatttttc acaaatafta ccagatecat caaaaccaag  
24001 caagaggtea ttattgaag atclactttt caacaaagt acacttgcag atgettggett  
24061 catcaaaaca tatggtgatt gccttggtga tattgetget agagacctca ttgtgcaca  
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24181 caacttctga ctgttagcgg gtacaatcac ttctggttgg accttgggtg caggtgctgc  
24241 attacaaata ccatttgeta tgcaaatggc ttatagggtt aatggtattg gagttacaca  
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25381 ataa

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***In silico* construct with Adenovirus vector shuttle containing CoV-2 Spike Protein gene**

```
1 taactataac ggtcctaagg tagcgaaagc tcagatctgg atctcccgat cccctatggt
61 cgactctcag tacaatctgc tctgatcccg catagttaag ccagtatctg ctcctgctt
121 gtgtgttga ggtcgctgag tagtgcgcg gcaaaattta agctacaaca aggcaaggct
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301 cgggggtcatt agttcatagc ccatatatgg agttccgcgt tacataactt acggtaaatg
361 gcccgcctgg ctgaccgccc aacgaccccc gccattgac gtcaataatg acgtatgttc
421 ccatagtaac gccaataggg actttccatt gacgtcaatg ggtggactat ttacggtaaa
481 ctgcccactt ggcatgacat caagtgtatc atatgccaag tacgccccct attgacgtca
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601 cttggcagta catctacgta ttatgcatcg ctattacat ggtgatgcgg ttttggcagt
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901 actatagggg gacccaagct ggctagcgtt taaacgggccc ctctagagtt gtggtttcaa
961 gtgatattct tgtaataaac taaacgaaca tgtttgtttt tcttgtttta ttgccactag tctctag
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122021 ggaaagttag ttacagattt attctagtgc gaataattgc acttttgaat atgtctctca
122081 gccttttctt atggaccttg aaggaaaaca gggttaattc aaaaatctta gggaatttgt
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```

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312| cccgacagga ctataaagat accagggcgtt tccccctgga agctccctcg tgcgctctcc  
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384| aataaaccca accgctacac cctgagcatc aaactctttt atcagttgga tcatgtcggc  
390| ggtgtcgcgg ccaagacggg cgagcttctt caccagaatg acatcacctt ctccacctt  
396| cactctcagc aaatccagcc ctcccgatc tgttgaactg ccggatgcct tgcggtaaa  
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552| catgagcgga tacatatgtt aatgtattta gaaaaataaa caaatagggg ttccgcgcac  
558| atttcccga aaagtccac ctgacgt

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**Artificial Spike Protein in Chinese patent (not found in any patient specimens)**

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tgcctgccc ggagaagaac taccaccg cccagccat ttgccagac 3300 ggcaaggccc acttccctag ggagggcgtg  
ttctgagca acgggacaca ctggttcgtg 3360 acccagcgga actttacga gcccagatt ataccacag ataacactt  
tgtgtccgg 3420 aactgcgatg tctgattgg gatcgtcaac aacacagtct acgacccct gcagcccgag 3480  
ctcgatagct ttaaggagga gctggataag tactttaaga accacacctc cctgatgtg 3540 gacctggggg atatcagcg  
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gagtcctga tcgacctgca ggagctggg 3660 aagtacgagc agtatcaaa gtggcctgg tacatctggc tgggttcat  
cgccgggctg 3720 atcgccatcg tgatgtgac cattatgctc tgctcatga ctactgctg ctctgctg 3780  
aagggtgtc gcagctgcg gagctgctc aagttgatg aggatgatg cgagccagt 3840 ctgaaggcg tgaagtgca  
ctacacctg aagctt

**Adenovirus 5 vector shuttle with Synthetic construct H7N9 HA gene 7640-9302**

1 taactataac ggtcctaagg tagcgaaagc tcagatctgg atctcccgat ccctatggt  
61 cgactctcag tacaatctgc tctgatgcc catagttaag ccagtatctg ctccctgctt  
121 gtgtgttga ggtcgtgag tagtgcgca gcaaaattta agctacaaca aggcaaggct  
181 tgaccgacaa ttgcatgaag aatctgctta gggtaggcg ttttgcgtg ctctcgatg  
241 tacgggccag atatacgcgt tgacattgat tattgactag ttattaatag taatcaatta  
301 cggggctcatt agttcatagc ccataatgg agttccgcgt tacataact acggtaaatg  
361 gccgcctgg ctgaccgccc aacgacccc gccattgac gtcaataatg acgtatgtc  
421 ccatagtaac gccaataggg acttccatt gacgtcaatg ggtggactat ttacggtaaa  
481 ctgccactt ggcagtacat caagtgtatc atatgccaag tacgcccct attgacgtca  
541 atgacggtaa atggccgcc tggcattatg ccagttacat gaccttatgg gactttccta  
601 ctggcagta catctacgta ttagtcacg ctattaccat ggtgatgcg ttttggcagt  
661 acatcaatgg gcgtggatag cggtttgact cacggggatt tccaagtct caccattg  
721 acgtcaatgg gagttgttt tggacccaaa atcaacggga cttccaaaa tctcgttaaca  
781 actccgccc attgacgcaa atgggcggtg ggcgtgtacg gtgggaggtc tatataagca  
841 gagctctctg gtaactaga gaaccactg ctactggct tategaaatt aatacgactc  
901 actataggga gacccaagct ggctagcgtt taaacgggcc ctctagagtt gtggtttcaa  
961 gtgatattct tgttaataac taaacgaac



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7681 tctgcctcgg acatcatgcc gtgtcaaacg gaaccaaagt aaacacatta actgaaagag  
7741 gagtggaagt cgtaatgca actgaaacag tggaacgaac aaacatcccc aggatctgct  
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7861 cacctcaatg tgaccaatc ctagaatctt cagccgattt aattattgag aggcgagaag  
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8161 gaaaaagccc agctctaata gtatggggga tccatcattc cgtatcaact gcagagcaaa  
8221 ccaagctata tgggagtga aacaaactgg tgacagttgg gatttctaat tatcaacaat  
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8341 ttcatggct aatgctaaat ccaatgata cagtcacttt cagtttcaat ggggctttca  
8401 tagctccaga cctgtcaagc ttctgagag gaaaatctat gggaatccag agtggagtag  
8461 aggttgatgc caattgtgaa ggggactgct atcatagtgg agggacaata ataagtaact  
8521 tgccatttca gaacatagat agcagggcag ttggaaaatg tccgagatat gtaagcaaa  
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8641 tatttggtgc tatagcgggt ttcatgaaa atggatggga aggcctaatt gatggttgg  
8701 atggtttcag acaccagaat gcacaggag agggaaactgc tgcagattac aaaagcactc  
8761 aatcggcaat tgatcaaata acaggaaaat taaaccggct tatagaaaa accaaccaac  
8821 aatttgagtt gatagacaat gaattcaatg aggtagagaa gcaaatcggg aatgtgataa  
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8941 tggagaacca gcatacaatt gatctggctg attcagaaat ggacaaactg tacgacagag  
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9121 acagggaaga ggaatgc aaatagaatac agatgaccc agtcaaaacta agcagcggc  
9181 acaagatgt gatactttgg tttagcttcg gggcatcatg ttcatactt ctaccattg  
9241 taatgggcct tgtcttcata tgtgtaaaga atggaaacat gcggtgcact attgtatat  
9301 aattg ccagccatct

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2521 gttgtttgcc cctccccctg gccttccttg accctggaag gtgccactcc cactgtcctt  
2581 tectaataaa atgaggaaat tgcctgcctt tgtctgagta ggtgtcattc tattctgggg  
2641 ggtgggggtgg ggcaggacag caagggggag gattgggaag acaatagcag gcctgtggg  
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3001 agcaaaaggc cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgttttcca  
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3241 gctttctcaa tgctacgct gtaggtatct cagtcgggtg taggtcgttc gctccaagct  
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3541 aaaaagagtt ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggttttt  
3601 tgtttgcaag cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt  
3661 ttctacgggg tctgacgctc agtggaacga aaactcacgt taagggattt tggcatgag  
3721 attatcaaaa aggatcttca cctagatcct ttgatactc cggcgttcag cctgtgccac  
3781 agccgacagg atggtgacca ccattgccc catatcaccg tcggtactga tcccgtcgtc  
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3961 catctcagc aaatccagcc ctcccgatc tgtgaactg ccggatgcct tgcggtaaa  
4021 gatgcggtta gcttttacc ctgcacttt gacgctgag gtctgcctc tgaagaaggt  
4081 gttgctgact cataccaggc ctgaatgcc ccatcatcca gccagaaagt gagggagcca  
4141 cggttgatga gagctttgtt gtaggtggac cagttggtga tttgaactt ttgctttgcc

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**Steven C. Quay, MD, PhD**

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4201 acggaacggt ctgcgttgtc gggaagatgc gtgatctgat ccttcaactc agcaaaagtt  
4261 cgatttattc aacaaagccg ccgtcccgtc aagtcagcgt aatgctctgc cagtgttaca  
4321 accaattaac caattctgat tagaaaaact catcgagcat caaatgaaac tgcaatttat  
4381 tcatatcagg attatcaata ccatattttt gaaaaagccg ttctgtaat gaaggagaaa  
4441 actcaccgag gcagttccat aggatggcaa gatcctggta tcggtctgcg attccgactc  
4501 gtccaacatc aatacaacct attaatctcc cctcgtcaaa aataaggtta tcaagtgaga  
4561 aatcaccatg agtgacgact gaatccggtg agaatggcaa aagcttatgc atttctttcc  
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4681 cgttattcat tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac  
4741 aattacaaac aggaatcgaa tgcaaccggc gcaggaacac tgccagcgcga tcaacaatat  
4801 ttacacctga atcaggatat tcttctaata cctggaatgc tgtttcccg gggatcgag  
4861 tggtagtaa ccatgcatca tcaggagtac ggataaatg ctgatggtc ggaagaggca  
4921 taaattccgt cagccagttt agtctgacca tctcatctgt aacatcattg gcaacgtac  
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5521 catgagcgga tacatatttg aatgtattta gaaaaataa caaatagggg ttccgcgcac  
5581 atttccccga aaagtgcac ctgacgt



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### Expression vector pShuttle-SN, complete sequence

GenBank: AY862402.1

[FASTA](#) [Graphics](#)

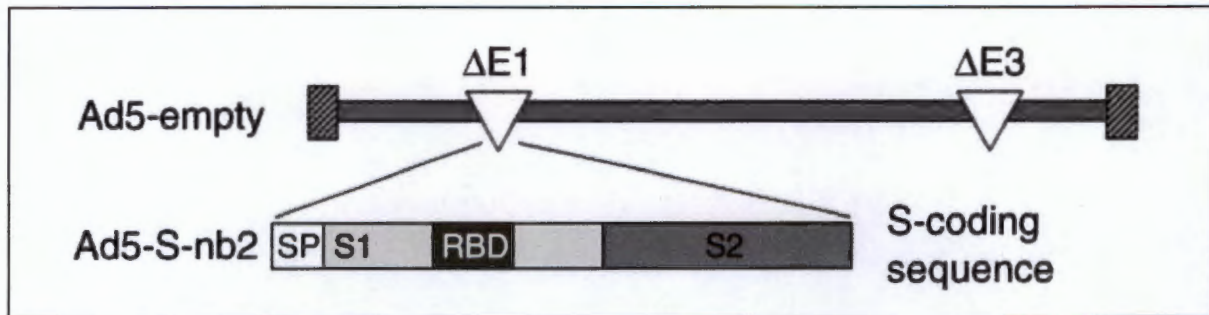
[Go to:](#)

LOCUS	AY862402	5607 bp	DNA	circular	SYN 19-JUL-2005
DEFINITION	Expression vector pShuttle-SN, complete sequence.				
ACCESSION	AY862402				
VERSION	AY862402.1				
KEYWORDS	.				
SOURCE	Expression vector pShuttle-SN				
ORGANISM	<a href="#">Expression vector pShuttle-SN</a>				
	other sequences; artificial sequences; vectors.				
REFERENCE	1 (bases 1 to 5607)				
AUTHORS	Liu,R.-Y., Wu,L.-Z., Huang,B.-J., Huang,J.-L., Zhang,Y.-L., Ke,M.-L., Wang,J.-M., Tan,W.-P., Zhang,R.-H., Chen,H.-K., Zeng,Y.-X. and Huang,W.				
TITLE	Adenoviral expression of a truncated S1 subunit of SARS-CoV spike protein results in specific humoral immune responses against SARS-CoV in rats				
JOURNAL	Virus Res. 112 (1-2), 24-31 (2005)				
PUBMED	<a href="#">16022898</a>				
REFERENCE	2 (bases 1 to 5607)				
AUTHORS	Liu,R.-Y., Huang,B.-J., Wu,L.-Z., Huang,J.-L., Zhang,R.-H., Zeng,Y.-X. and Huang,W.				
TITLE	Constructing recombinant adenovirus carrying the spike gene fragments as a vaccine against SARS-CoV by in vitro ligation				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 5607)				
AUTHORS	Liu,R.-Y., Huang,B.-J., Wu,L.-Z., Huang,J.-L., Zhang,R.-H., Zeng,Y.-X. and Huang,W.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-DEC-2004) Cancer Center, Sun Yat-Sen University, 651 Dongfeng Road East, Guangzhou, Guangdong 510660, China				
FEATURES	Location/Qualifiers				
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	/mol_type="other DNA"				
	/db_xref="taxon:308969"				
	/country="China"				
CDS	990..2507				
	/codon_start=1				
	/translation_table=11				
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	/protein_id="AAW56614.1"				
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misc_feature	990..2459				
	/note="Region: SARS coronavirus spike glycoprotein"				
misc_feature	2460..2507				
	/note="derived from pShuttle vector"				

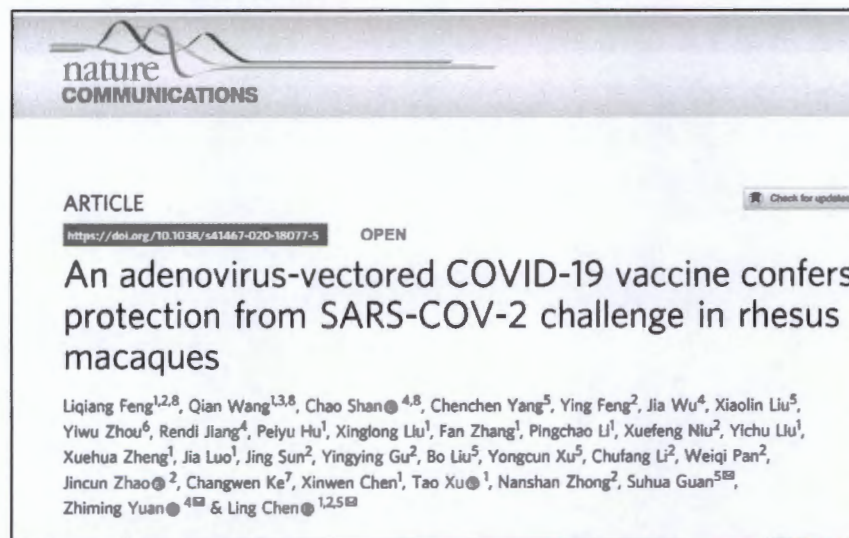
Source: <https://www.ncbi.nlm.nih.gov/nuccore/AY862402.1?report=GenBank>

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**Steven C. Quay, MD, PhD**

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Source: <https://www.nature.com/articles/s41467-020-18077-5>



# Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

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Adenovirus vaccine sequences in patient specimen WIV02 from patient who is 32 y, male, hospitalized, ICU4G, outbreak 19 Dec 2019.

**SRX7730880: RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
1 ILLUMINA (Illumina HiSeq 3000) run: 67.1M spots, 20.1G bases, 12.6Gb downloads

**Design:** Total RNA was extracted from bronchoalveolar lavage fluid using the QiAamp Viral RNA Mini Kit (50) following the manufacturers instructions. An RNA library was then constructed using the MGIEasy RNA Library Prep Set (96 RXN) (Cat. No.: 1000006384). Paired-end (150 bp) sequencing of the RNA library was performed on the MGISEQ-2000RS platform.

**Submitted by:** Wuhan Institute of Virology, Chinese Academy of Sciences

**Study:** Severe acute respiratory syndrome coronavirus 2 Raw sequence reads  
[PRJNA605883](#) • [SRP248613](#) • [All experiments](#) • [All runs](#)

[Hide Abstract](#)  
Discovery and characterization of a novel human coronavirus from five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak.

**Sample:**  
[SAMN14062198](#) • [SR56151291](#) • [All experiments](#) • [All runs](#)  
Organism: [Severe acute respiratory syndrome coronavirus 2](#)

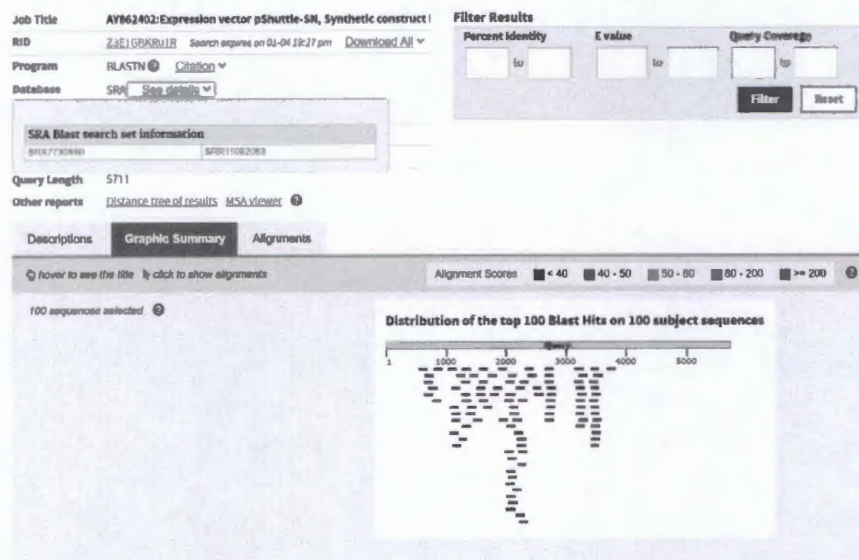
**Library:**  
Name: WIV02-2  
Instrument: Illumina HiSeq 3000  
Strategy: RNA-Seq  
Source: METAGENOMIC  
Selection: RANDOM  
Layout: PAIRED

**Runs:** 1 run, 67.1M spots, 20.1G bases, 12.6Gb

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR11092063</a>	67,083,195	20.1G	12.6Gb	2020-02-16

URL: <https://www.ncbi.nlm.nih.gov/sra/SRX7730880%5baccn%5d>

Adenovirus Expression vector pShuttle-SN, Synthetic construct H7N9 HA gene 7640-9302

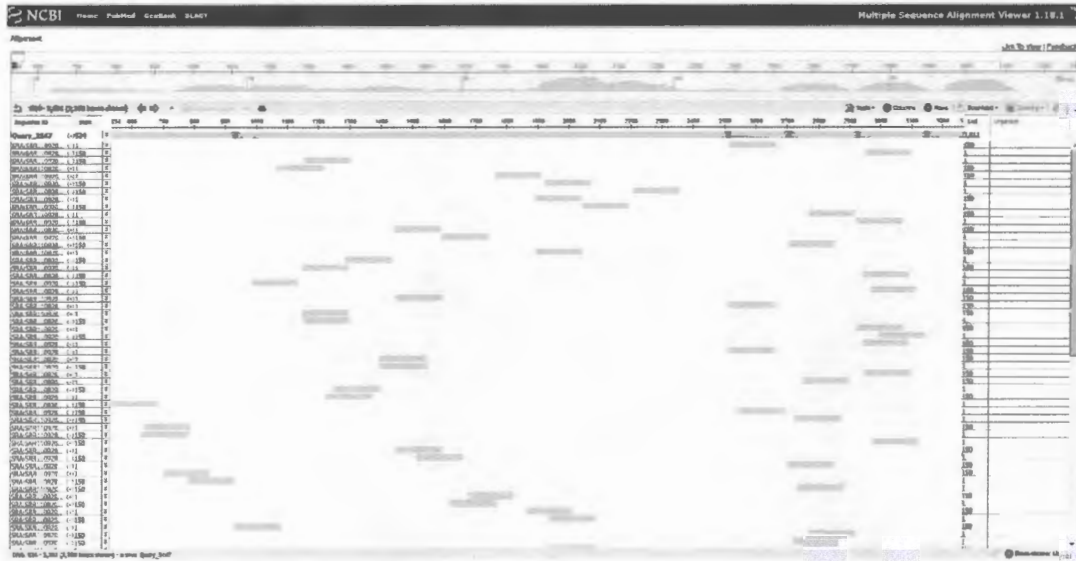


534-3301 contiguous nt sequence (2768 nt) in H7N9 HA gene

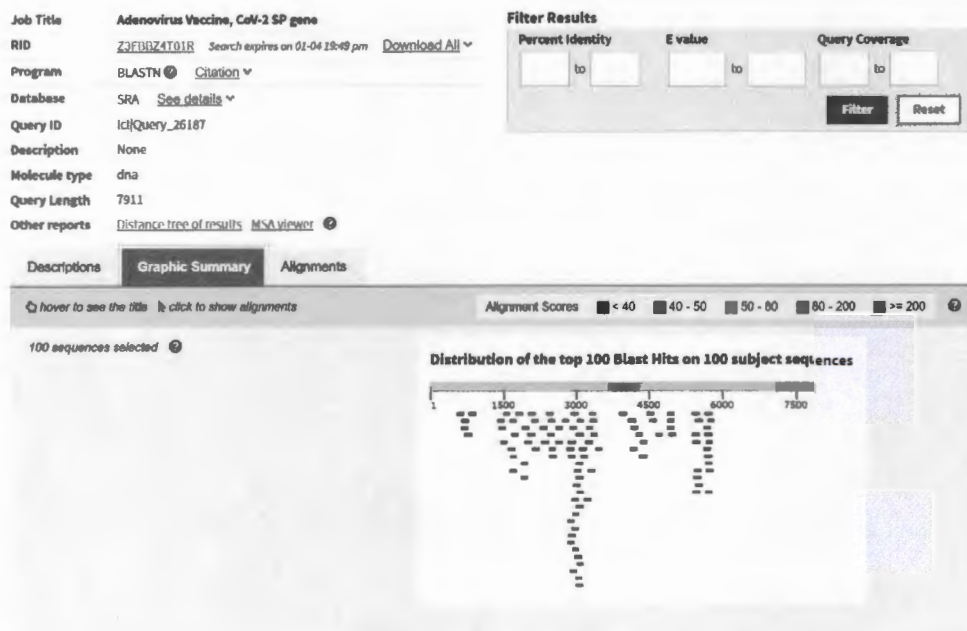


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## Adenovirus with CoV-2 Spike Protein, full sequence



534-4573 contiguous (4040 nts)

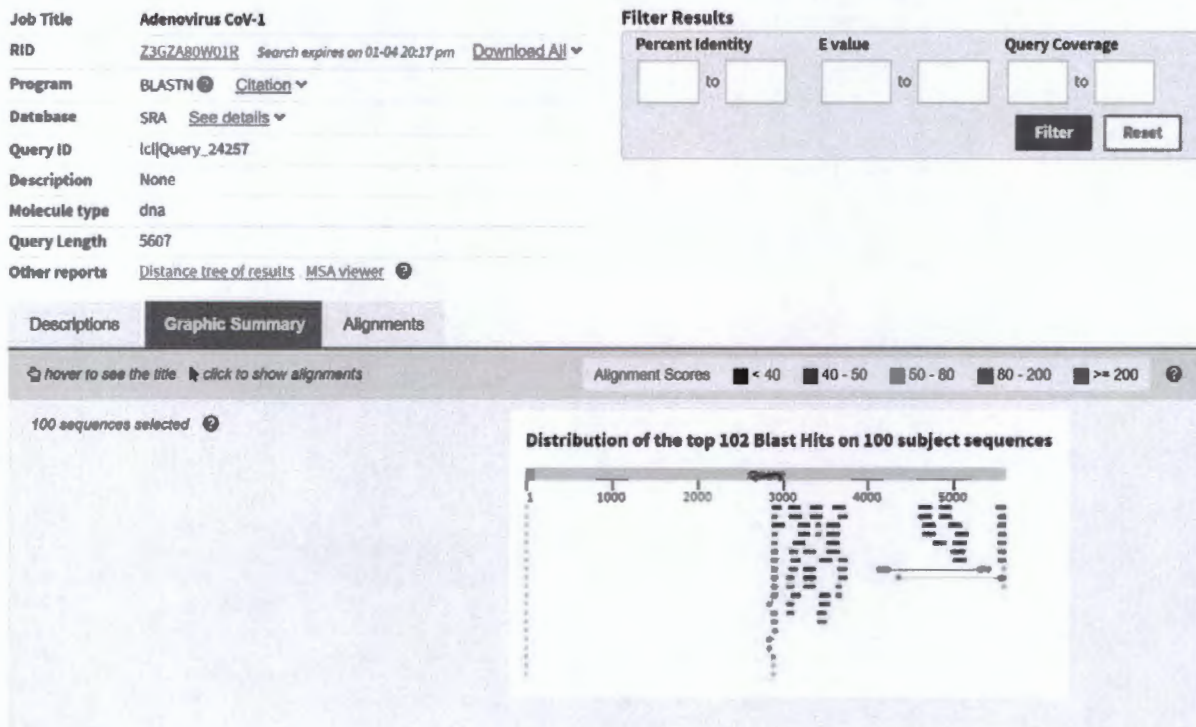
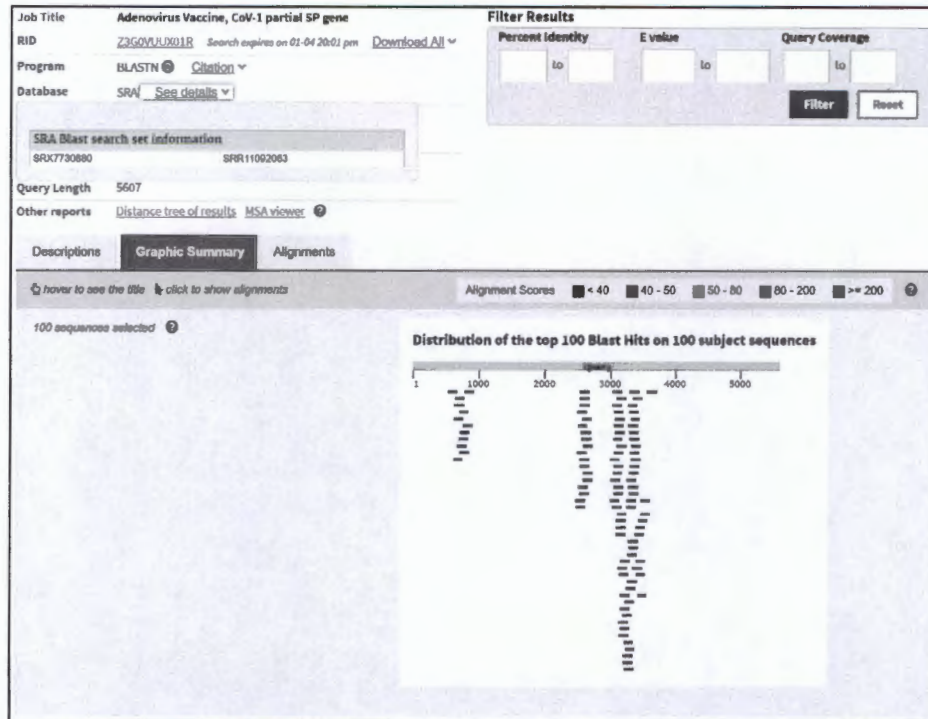
Adenovirus with CoV-1 partial sequence

534-1905 (1372 nts) contiguous

## Bayesian Analysis of SARS-CoV-2 Origin

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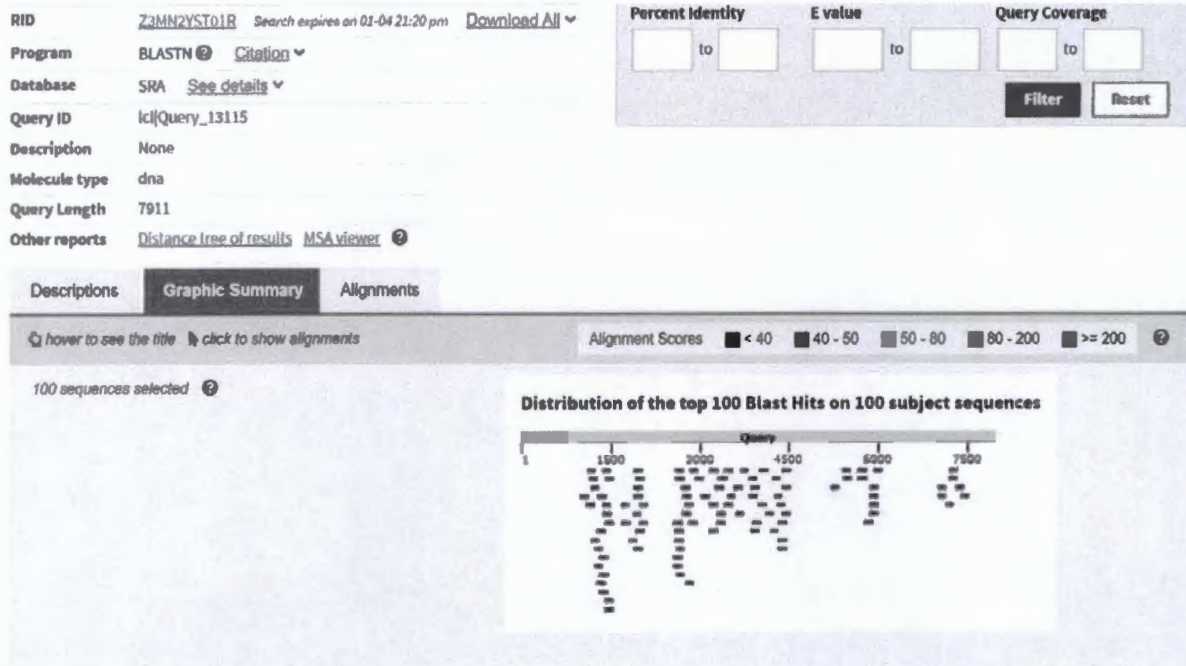


Adenovirus vaccine with CoV-2 SP:

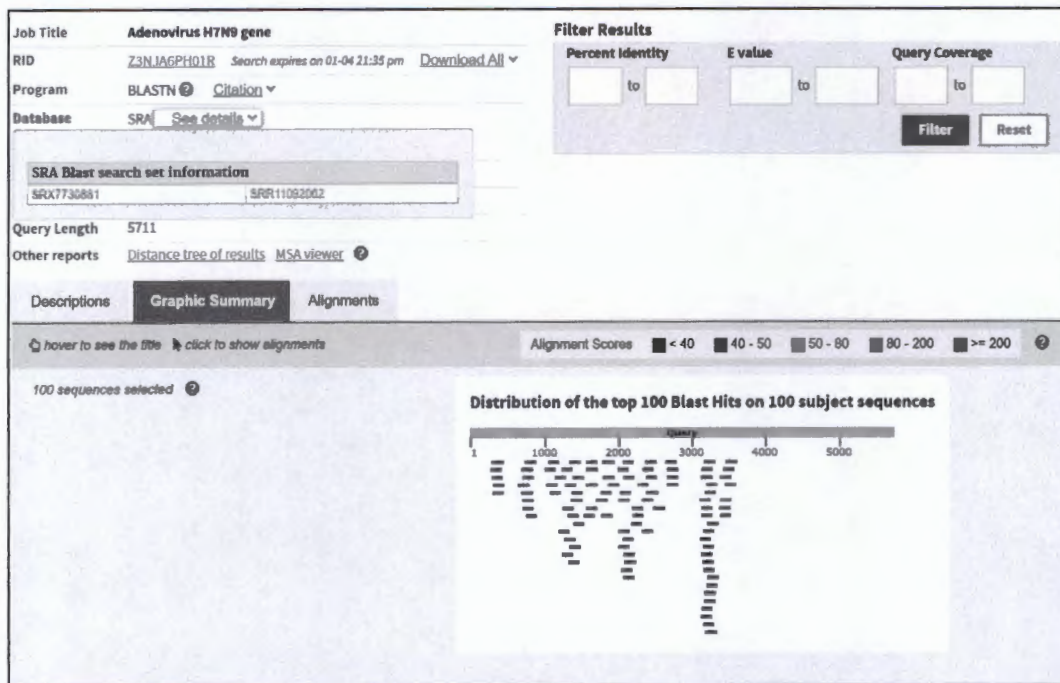
## Bayesian Analysis of SARS-CoV-2 Origin

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## Adenovirus H7N9



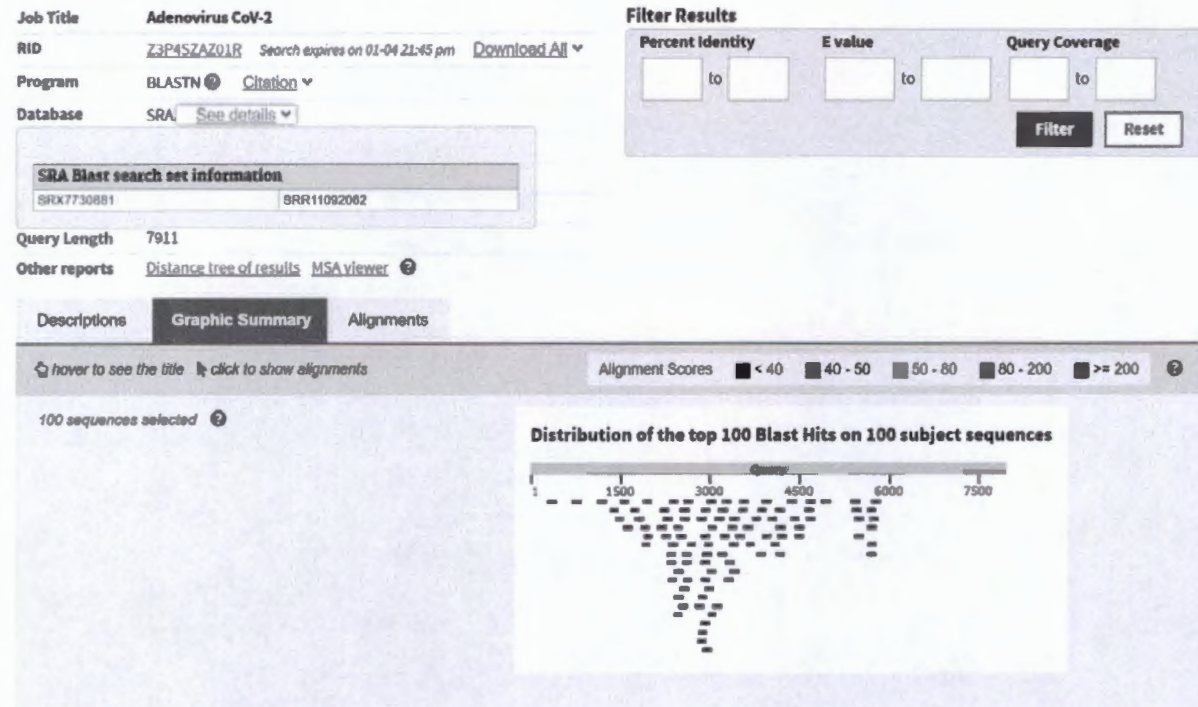


## Bayesian Analysis of SARS-CoV-2 Origin

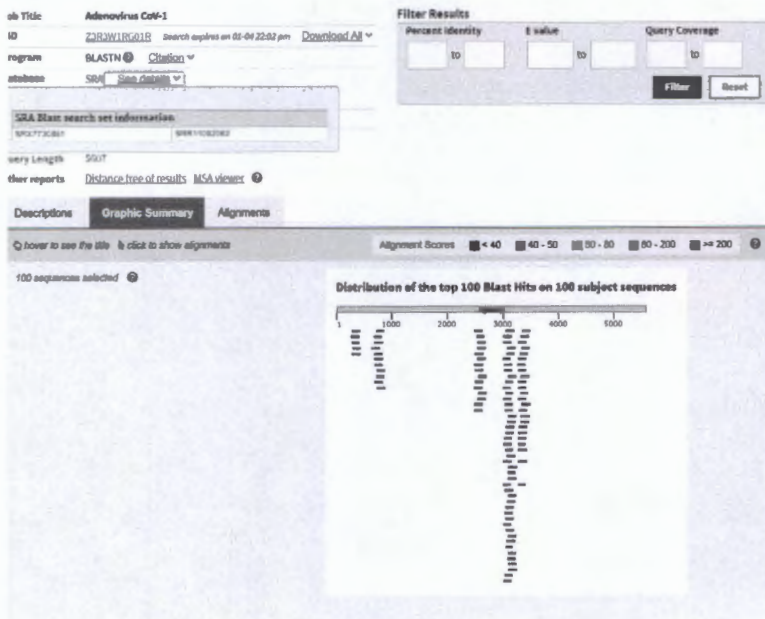
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### Adenovirus CoV-2



### Adenovirus CoV-1

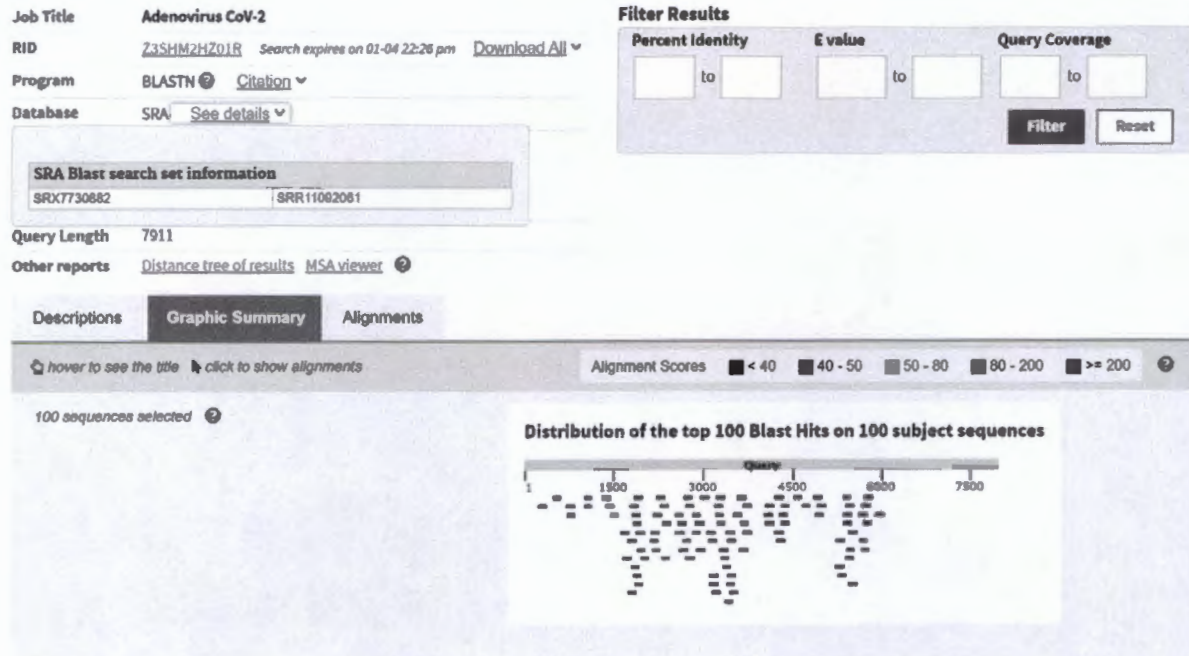


# Bayesian Analysis of SARS-CoV-2 Origin

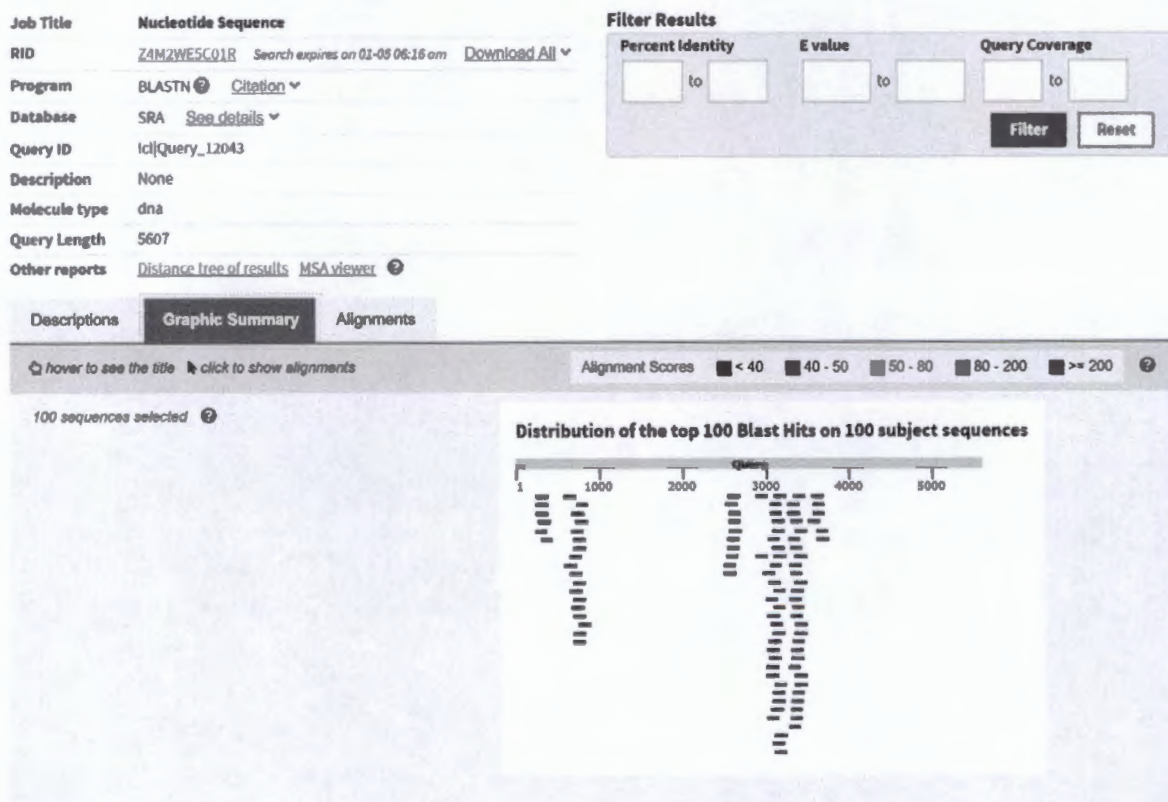
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## Adenovirus CoV-2



## WIV-7 patient blast with Adenovirus to CoV-1





Bayesian Analysis of SARS-CoV-2 Origin  
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**Blast analysis of early RNA seq raw reads from the Wuhan Institute of virology contain extensive reads matching “Expression vector pShuttle-SN” sequences, the same adenovirus vector used by the PLA Army for the creation of a vaccine.**

Following the 2003 SARS epidemic, Liu et al. developed an adenoviral expression vector of a truncated S1 subunit of SARS-CoV spike protein that resulted in specific humoral immune responses against SARS-CoV in rats.<sup>143</sup> This same vector was used to create the CoV-2 adenovirus vector vaccine.<sup>144</sup>

In order to test the hypothesis that CoV-2 began in the PLA Hospital as a vaccine challenge clinical trial that went awry, RNA-Seq raw reads from nasopharyngeal specimens of Wuhan COVID patients were blasted against the published genome sequence of the SARS-CoV-1 vaccine (GenBank [AY862402.1](#)). I used the SARS-CoV-1 vaccine because the PLA CoV-2 vaccine has not been published.

Nt Sequence	Function
1-990	Adeno virus genes
991-2506	Truncated N-terminus of SARS-CoV-1 Spike Protein
2507-5607	Adeno virus genes

The expected result would be the finding of RNA-Seq sequence raw reads that were homologous to the two Adenovirus regions but only partially homologous (about 80%) to the SARS-CoV-1 regions.

Eleven entries were found on GenBank of SRA data for RNA-Seq of early COVID-19 patients from Wuhan that were sequenced at either the WIV or the Hubei Provincial Center for Disease Control and Prevention (Hubei CDC). These entries are in the Text-Table below.

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<sup>143</sup> <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7114075/>

<sup>144</sup> Chinese patent, attached herein.



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- ☐ **RNA-Seq of Homo sapiens: hCov-19 infected patients Bronchoalveolar lavage uid**  
1. 1 ILLUMINA (Illumina MiSeq) run: 5.8M spots, 1.7G bases, 634.3Mb downloads  
Accession: SRX8032203
- ☐ **RNA-Seq of Homo sapiens: hCov-19 infected patients Bronchoalveolar lavage uid**  
2. 1 ILLUMINA (Illumina MiSeq) run: 5.2M spots, 1.6G bases, 583.4Mb downloads  
Accession: SRX8032202
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
3. 1 ILLUMINA (Illumina MiSeq) run: 5.2M spots, 1.5G bases, 772.9Mb downloads  
Accession: SRX7730887
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
4. 1 ILLUMINA (Illumina MiSeq) run: 5.2M spots, 1.5G bases, 768.3Mb downloads  
Accession: SRX7730886
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
5. 1 ILLUMINA (Illumina MiSeq) run: 8.3M spots, 2.2G bases, 1.2Gb downloads  
Accession: SRX7730885
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
6. 1 ILLUMINA (Illumina HiSeq 3000) run: 38.5M spots, 11.5G bases, 7.1Gb downloads  
Accession: SRX7730884
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
7. 1 ILLUMINA (Illumina HiSeq 3000) run: 29.7M spots, 8.9G bases, 5.6Gb downloads  
Accession: SRX7730883
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
8. 1 ILLUMINA (Illumina HiSeq 3000) run: 34.3M spots, 10.3G bases, 6.4Gb downloads  
Accession: SRX7730882
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
9. 1 ILLUMINA (Illumina HiSeq 1000) run: 61.3M spots, 18.4G bases, 11.4Gb downloads  
Accession: SRX7730881
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
10. 1 ILLUMINA (Illumina HiSeq 3000) run: 67.1M spots, 20.1G bases, 12.6Gb downloads  
Accession: SRX7730880
- ☐ **RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
11. 1 ILLUMINA (Illumina MiSeq) run: 3.6M spots, 1G bases, 548.1Mb downloads  
Accession: SRX7730879

The WIV entry with the greatest read depth, Number 10 above, is described below:

# Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021

**SRR11092083: RNA-Seq of Homo sapiens: bronchoalveolar lavage fluid**  
1 ILLUMINA (Illumina HiSeq 3000) run: 67.1M spots, 20.1G bases, 12.6Gb downloads

**Design:** Total RNA was extracted from bronchoalveolar lavage fluid using the QIAamp Viral RNA Mini Kit (50) following the manufacturers instructions. An RNA library was then constructed using the MGIEasy RNA Library Prep Set (96 RXN) (Cat. No.: 1000006384). Paired-end (150 bp) sequencing of the RNA library was performed on the MGISEQ-2000RS platform.

**Submitted by:** Wuhan Institute of Virology, Chinese Academy of Sciences

**Study:** Severe acute respiratory syndrome coronavirus 2 Raw sequence reads  
[PRJNA605983](#) • [SRP249613](#) • [All experiments](#) • [All runs](#)  
[show Abstract](#)

**Sample:**  
[SAMN14082199](#) • [SRS6151291](#) • [All experiments](#) • [All runs](#)  
Organism: [Severe acute respiratory syndrome coronavirus 2](#)

**Library:**  
Name: WIV02-2  
Instrument: Illumina HiSeq 3000  
Strategy: RNA-Seq  
Source: METAGENOMIC  
Selection: RANDOM  
Layout: PAIRED

**Runs:** 1 run, 67.1M spots, 20.1G bases, 12.6Gb

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR11092083</a>	67,083,195	20.1G	12.6Gb	2020-02-16

Unexpectedly, over 100 sequences producing significant alignment were identified:

BLAST -> blastn suite-SRA -> results for RID-S76CAHY0018

Home Recent Results Saved Strategies Help

< Edit Search Save Search Search Summary

Job Title [gh|AY862402.1](#)

RID [S76CAHY0018](#) Search expires on 10-31 07:47 am Download All

Program BLASTN C-Region

Database SRA See details

Query ID [AY862402.1](#)

Description Expression vector pShuttle-SH, complete sequence

Molecule type nucleic acid

Query Length 5607

Other reports Distance tree of results MSA viewer

Filter Results

Percent identity E value Query Coverage

to to to

Filter Reset

Descriptions Graphic Summary Alignments

Sequences producing significant alignments

Download Manage Columns Show 100

☒ select all 100 sequences selected

Graphics Distance tree of results

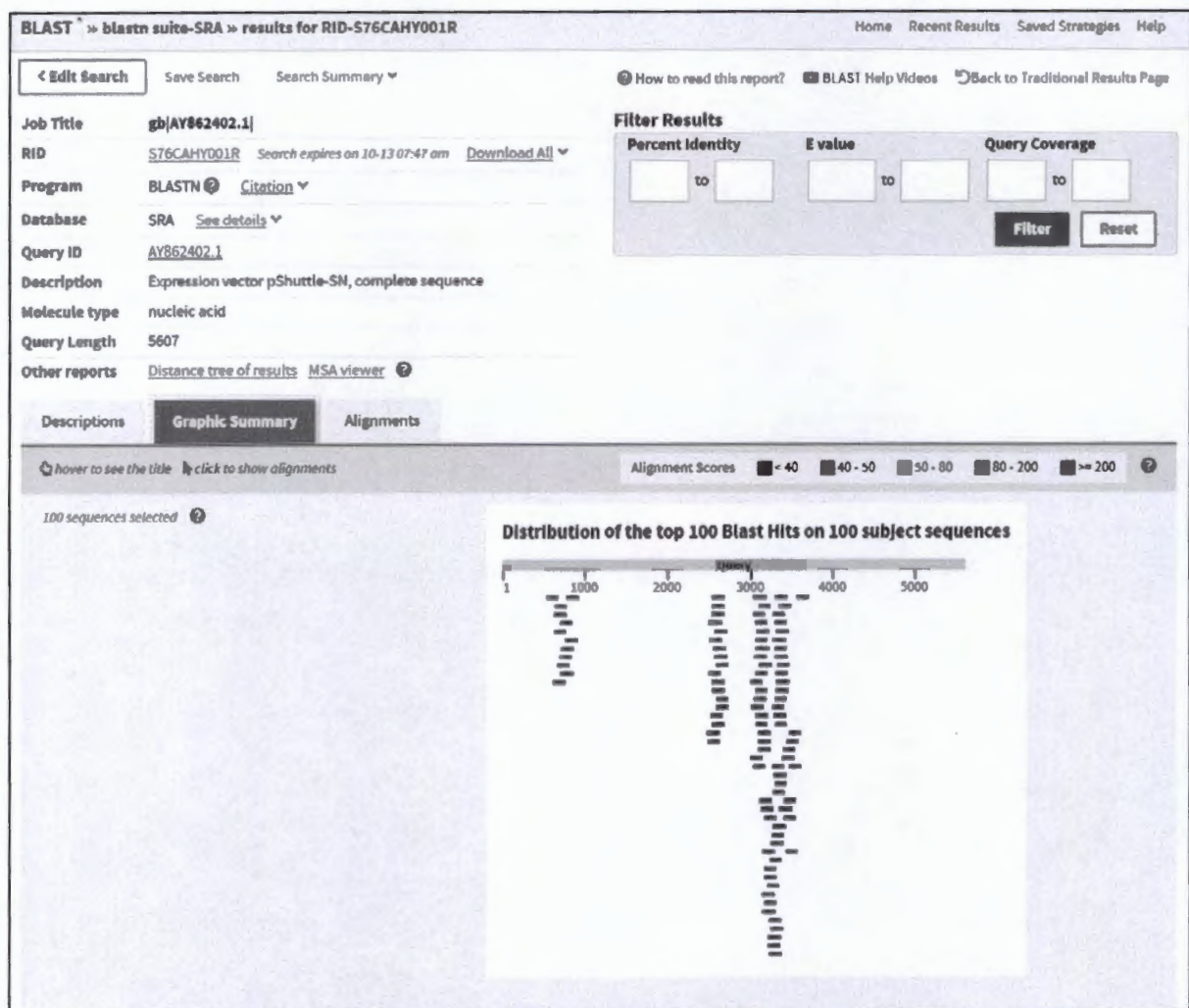
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> <a href="#">SRR11092083.69004460.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.69004460.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.69452078.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.69452078.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.69120999.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.69120999.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.63120099.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.63120099.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.62730385.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.62730385.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.61100039.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.61100039.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.60748775.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.60748775.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.60011402.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.60011402.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.59195252.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.59195252.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.59116526.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.59116526.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.60126683.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.60126683.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.61751550.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.61751550.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.67484454.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.67484454.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.59079036.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.59079036.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.60086194.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.60086194.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.59085408.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.59085408.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.65111993.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.65111993.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.53777284.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.53777284.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.53079613.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.53079613.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.62085281.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.62085281.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.61414106.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.61414106.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.61010881.2</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.61010881.2</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.60060437.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.60060437.1</a>
<input checked="" type="checkbox"/> <a href="#">SRR11092083.53609771.1</a>	278	278	2%	2e-70	100.00%	<a href="#">SRR11092083.53609771.1</a>



**Bayesian Analysis of SARS-CoV-2 Origin**  
**Steven C. Quay, MD, PhD**

29 January 2021

A graphical display of the alignments shows they are not in the Spike Protein region (961 to 2507) of the adenovirus vector but outside of those regions.



An examination of individual reads shows 100% homology over the entire 150 nt segments and outside of the Spike Protein region. The first set of reads are immediately downstream of the Spike Protein segment. The other read is from the 5' boundary of the Adenovirus vector with the Spike Protein region.





## Bayesian Analysis of SARS-CoV-2 Origin

Steven C. Quay, MD, PhD

29 January 2021

To test if this was the actual SARS-CoV-1 vaccine vector and had been given to the patients as an desperate attempt to create immunity during an infection, the Spike Protein region of the vaccine was blasted against the above sample, looking for a near 100% homology. The only reads were a 38 nt segment of 1482-1518, with one gap, as expected. The absence of long reads for the SARS-CoV-1 Spike Protein establishes that this vaccine was not a CoV-1 vaccine.

To test if the homology seen between lavage specimens of patients in Wuhan with the CoV-1 Adenovirus vaccine was due to homology with human sequences, the Expression vector itself was blasted against *Homo sapien* sequences, but no matches were found, as shown below.

BLAST » blastn suite » results for RID-S793VKCV01R

[← Edit Search](#) [Save Search](#) [Search Summary](#) ▼

**i** Your results are filtered to match records that include: *Homo sapiens* (taxid:9606)

Job Title **AY862402:Expression vector pShuttle-SN, complete...**

RID [S793VKCV01R](#) Search expires on 10-13 08:34 am [Download All](#) ▼

Program [Citation](#) ▼

Database nt [See details](#) ▼

Query ID [AY862402.1](#)

Description Expression vector pShuttle-SN, complete sequence

Molecule type nucleic acid

Query Length 5607

Other reports [?](#)

**A** No significant similarity found. For reasons why, [click here](#)